

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 25, 2003, 08:33:12 : Search time 1051 Seconds
(without alignments)
12857.212 Million cell updates/sec

Title: us-09-831-000-1

Perfect score: 40000
Sequence: 1 gacgcgggaaacgcgagcg999.....accttatgataactcgttt 40000

Scoring table: OLIGO-NUC
Gapop 60.0 , Gapext 60.0

Number of hits satisfying chosen parameters: 378376

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : GB_VI:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40000	100.0	133719	1 AF083501	AF083501 Macaca mu
2	10772	26.9	130733	1 AF210726	AF210726 Macaca mu
3	7957	19.9	10595	1 AF029302	AF029302 Rhesus ma
4	3804	9.5	3804	1 AF087411	AF087411 Rhesus ma
5	475	1.2	475	1 AF159033	AF159033 Macaque g
6	331	0.8	395	1 AF159041	AF159041 Macaque g
7	106	0.3	320	1 AF159040	AF159040 Macaque g
8	80	0.2	2708	1 AF204167	AF204167 Macaca ne
9	71	0.2	475	1 AF159031	AF159031 Macaque g
10	56	0.1	336	1 AF159034	AF159034 Macaque g
11	50	0.1	475	1 AF159032	AF159032 Macaque g
12	48	0.1	336	1 AF159036	AF159036 Macaque g
13	48	0.1	336	1 AF159037	AF159037 Macaque g
14	47	0.1	336	1 AF159035	AF159035 Macaque g
15	46	0.1	3144	1 SHIDNAPOLA	L24487 Pseudorabies
16	41	0.1	336	1 AF159038	AF159038 Macaque g
17	38	0.1	475	1 AF282937	AF282937 Mandrillu
18	38	0.1	475	1 AF282938	AF282938 Mandrillu
19	38	0.1	475	1 AF282939	AF282939 Mandrillu
20	38	0.1	475	1 AF282940	AF282940 Mandrillu
21	33	0.1	130733	1 AF210726	AF210726 Macaca mu
22	33	0.1	133719	1 AF083501	AF083501 Macaca mu
23	32	0.1	454	1 CRH251574	AJ251574 Chloroceb
24	31	0.1	523	1 AT237372	AT237372 Caprine h
25	29	0.1	395	1 AF159039	AF159039 Macaque g
26	29	0.1	469	1 AF031811	AF031811 Bovine he
27	29	0.1	3638	1 AF005477	AF005477 Kaposi's
28	29	0.1	108873	1 AF318573	AF318573 Bovine he
29	29	0.1	133661	1 U93872	U93872 Kaposi's sa
30	29	0.1	137508	1 KSU75698	KSU75698 Kaposi's sa
31	27	0.1	480	1 AF031808	AF031808 Bovine ly
32	27	0.1	1295	1 AF327830	AF327830 Bovine ly
33	26	0.1	475	1 AF005478	AF005478 Retroperi

34	26	0.1	3554	1 AF204166	AF204166 Retroperi
35	23	0.1	475	1 AF250880	AF250880 Pan trogl
36	23	0.1	1297	1 AF327831	AF327831 Ovine her
37	23	0.1	1339	1 AF275657	AF275657 Badger he
38	23	0.1	6165	1 AF376034	AF376034 Badger he
39	23	0.1	184427	1 EHVU20824	U20824 Equine herp
40	22	0.1	171096	1 AV037858	AV037858 Cercopit
41	21	0.1	949	1 AF292063	AF292063 Cercopit
42	21	0.1	3623	1 AF283477	AF283477 Caprine h
43	21	0.1	12708	1 AF033822	AF033822 Walleye d
44	21	0.1	12708	1 TYCAG	LA1838 Walleye der
45	21	0.1	130608	1 AF005370	AF005370 Alcelaphi

ALIGNMENTS

RESULT 1	AF083501	133719 bp	DNA	linear	VRL 26-JUN-2000
LOCUS	AF083501				
DEFINITION	Macaca mulatta rhadinovirus 17577, complete genome.				
ACCESSION	AF083501				
VERSION	AF083501.3	GI:8714565			
KEYWORDS					
SOURCE					
ORGANISM	Macaca mulatta rhadinovirus 17577				
REFERENCE	Macaca mulatta rhadinovirus 17577				
AUTHORS	Sealies,R.P., Bergquam,E.P., Axthelm,M.K. and Wong,S.W.				
TITLE	Sequence and genomic analysis of a Rhesus macaque rhadinovirus with similarity to Kaposi's sarcoma-associated herpesvirus/human herpesvirus 8				
JOURNAL	J. Virol. 73 (4), 3040-3053 (1999)				
MEDLINE	99174001				
PUBMED	10074154				
REFERENCE	2 (bases 1 to 133719)				
AUTHORS	Sealies,R.P., Bergquam,E.P., Axthelm,M.K. and Wong,S.W.				
TITLE	Direct Submission				
JOURNAL	Submitted (11-AUG-1998) Division of Pathobiology and Immunology, Oregon Health Sciences University/ Oregon Regional Primate Research Center, 505 NW 185th Avenue, Beaverton, OR 97006, USA				
REFERENCE	3 (bases 1 to 133719)				
AUTHORS	Sealies,R.P., Bergquam,E.P., Axthelm,M.K. and Wong,S.W.				
TITLE	Direct Submission				
JOURNAL	Submitted (16-JUL-1999) Division of Pathobiology and Immunology, Oregon Health Sciences University/ Oregon Regional Primate Research Center, 505 NW 185th Avenue, Beaverton, OR 97006, USA				
REFERENCE	4 (bases 1 to 133719)				
AUTHORS	Sealies,R.P., Bergquam,E.P., Axthelm,M.K. and Wong,S.W.				
TITLE	Direct Submission				
JOURNAL	Submitted (26-JUN-2000) Division of Pathobiology and Immunology, Oregon Health Sciences University/ Oregon Regional Primate Research Center, 505 NW 185th Avenue, Beaverton, OR 97006, USA				
REMARK	Sequence update by submitter				
COMMENT	On Jun 26, 2000 this sequence version replaced gi:5508840.				
FEATURES					
source	Location/Qualifiers				
	1..133719				
	/organism="Macaca mulatta rhadinovirus 17577"				
	/mol_type="genomic DNA"				
	/db_xref="taxon:93534"				
	1..840				
	/note="partial terminal repeat"				
CDS	/codon_start=1				
	/product="R1"				
	/protein_id="AAD21330.1"				
	/db_xref="GI:4494908"				
	/translation="MFVLYELMLQPPVSVLLPAKRTSVPTMCPHREDYTLTGRCGTSTANDSTQFMFNNTLVKSGNFTGRVLSVTPNATISQVACQRTTKTRNNIDFRVSSRLTQERSSGYTYANNRVRGCVSGGVTLRNVFHLNGTAVINGTNTNHTFVLTERTGTGTFPCSAFIGNEKFSQRTINVEFTSFTRKPTNDIPNESHFNKGTQIOOTASV				

CDS

ORPENYVPSVPFISGVLITGIAISLINCMLTTCINCENSESTSYASQTSYIQPSH
NORNTNCSRHITTKNAHOSESIEELPNQHSSETSCQVLLEVKNAVADSPQNTI
NEMEQYDVVVKNI EQTSYEDNVEMHDSIDINPNFNYSGLILEEDEVFNYELEN
OYHGILLENLDHNEYNHLNMLNMEQYDWLE"
complement(2692..3258)
/note="ORF 2: similar to Kaposi's sarcoma-associated
herpesvirus ORF 2"
/codon_start=1
/product="dihydrofolate reductase"
/protein_id="AAd21331.1"
/db_xref="GI:4494909"

CDS

/translation="MDITVNCIAVDEBOLGIGKNGTMPRLNEMMYFOKMTSPSV
VGEKNVVMKGRKTSPEKREPLVNRINIILSRLEKREPHAHPLARDIDAFNFR
OYKKEQLTVMYIGKSYFESVLNKCPLKLYTRIMESFDCDVFPSINTEYTM
SEIKQDNFEENGIRKYKFOYKFNK"
3676..5613
/note="ORF 4: similar to Kaposi's sarcoma-associated
herpesvirus ORF 4"
/codon_start=1
/product="complement binding protein"
/protein_id="AAd21332.1"
/db_xref="GI:4494910"

CDS

/translation="MTFLFLPLFLHAIYVHCDECKPHEFTEYKVSNTKEDLYS
GETALICRPGVNTKILITTECLONGTMSPTNPPCDKRCPTPADLINGAHIHGD
NALKGSNIYECNNGSYDLISGNVRPCLODNEPNSPEVCEIOCRPAVHNG
DYLPNQDYNNGDATTFCOSLSYTVIGSTTVLCISNKRKNSFPICLMLVCSPIDN
GTYDGLSRNNGQSTIVKSCSDGYNIVGPELTCTNTWPELPCVLYLNNPQIM
PETPEPTPDYOKINLSTAKTATPNAFVTVVSPKDDTCVAPHERHVAEN
DEKETSVASVELICRPGFTKQSTVSECLNGTWTAIPNAKCHRRKCPTEPDLN
YVTSGEDAFKGTNITKYCNQYOLGSMRIGLKDOLKTVDEKAPACIDITCK
PPOITNGKHYHVDFOYLDIVFSCNDRSLDEMTKCSINTMTCISNPPCDEITC
SAPNIAHKLITGSSSVYKIGOSVITGCEGTGLIGSEITCKDSSMPPLEPTCPAY
SMSPTEKPEKNTPEAPKPNTPVNGHTPKPPPNPPIAPPMKMRHVLY
LEASVALFLVLAALYCCFLK"
6045..9443
/note="ORF 6: similar to Kaposi's sarcoma-associated
herpesvirus ORF 6"
/codon_start=1
/product="ssDNA binding protein"
/protein_id="AAd21333.1"
/db_xref="GI:4494911"

CDS

/translation="MASKNGGPLEDNOGRAPIGAGGYVAYKODEPFAEASILG
NRSGSVFSLPIYGLTVHEHNEPLTVKAAKXKVTDTLVAVKVCHEHREIVFNAST
FRPYDGTGLNELCEARALRGYTFIERGPHSTWNPBECQOLDKDEMPAGVYTE
GFERLMRGCLVPAVFOVOOIAGRQAFKVLVDEDLFAPGRHMPREYHNDVAVL
YDLSFTSIAQALRLKADVAVIHAIEKQPMODHYKIAKIVQAQFSTLPKTDGSHM
IVDSVVALALSYCGMFECPDACLNDYSMPLFDCDSPEARVNALEMSAQAV
HVAQGLFANSLVLYTKVOKAPRGOKGDVNVNSFLOHGGFLNEATIKENGSEAF
KGVNSALDSSFPYHLYAASPSHLAKLYCMOFLQHHKSTNOAFNMVHYGT
AANSKCTLCGNTPATCLNTLFLKDRFPVATTPQRDPVTVGTGTFNDELIG
NFASRDEEDGNPADEHPKTYWOLCQTVTERKSAIGITTEDHNMVNLINIOSELR
VEKIDISIVDEVKFMVSMIKNNFNREHVSYHIILOFCNVAQAQCAVFLVLY
KSLMIIODICLPCMIYEODNPAMGILPEMLKMFOTLNTFNKACLDLGVCE
LKIVHROGCEPFDNAGNGMAPEKMOVARARAMVVPKSIKINRIITFSNTGSE
AVOGSEVPCGTGROVYVAGPYMKTLNHLARPDTKALYIMHKISQNTKTVLK
DVPDELAELVYKTNLSLAFEBETVLDVDPDSLSYKRIKNGAILNACGDIQYAT
TLHCTFVLQTIIDEEPHYLGSAAIATPAVYLAIRGTLATVQTTARQPAAGRL
RPVITPVAVNKKYGVNGNNVFNHCGNLGYPAGRGVDNRPBESSPEKTKGSALRK
RHVMATPIIDRLIKAAQOTISTFEASVRSVQALLKEDKNPNLKSYLELHILG
KGCODLSEDOYVLYGDYCM/LDEVLF/LDINAOGCVPTWTEADGALIEDQDADLO
FVDSDDITATSCQPEBOLPTPSAGALLAGKKRKNALSLDL"
9468..11528
/note="ORF 7: similar to Kaposi's sarcoma-associated
herpesvirus ORF 7"
/codon_start=1
/product="transport protein"
/protein_id="AAd21334.1"
/db_xref="GI:4494912"

CDS

/translation="MAITNRERLLRANVIAITGAVENYTPKGAATTAKPPPG
SPTPEPMPRAEAFKFRCSATGELEFRLEKCEGTEDEKIOEELIMWEKKNIV
PHIFKVRKRYATSVIYRGWETAVNGKQVIRAPVOYEINHDYTYOCSSMRV
VNGIYNTYDRFTNQYFLOQREBELTNIOYFESQVLYTTPGPGCITYRRTVNC
ETVMDIANSABEYSTYVTAIGDVEVSPCHNDSTCSVAEKTENGLARVLNTIYD
FATROPTEPTEVFAOSGEYVSWKAKEDRSACALTLTKTPRALIQTHEASVYHVN
DVTATFTSPLSQVNTGTGYPCLNDINQITLNAITKLSDTNATGSDQYETEGELF
LIMQULTEPLSLADEMRNGTTPAPPTTSTANRYRSGVTEAOATDILAQLOFAY
DKLRASINKVLELSRAMCREQVDTYMMWELSKINPSVMAIYGRVSAFVGDAT
SVTDCAVADQASVSTHKSIRTSPTGICYSRPVTPREINSTLTFKGOIGPRAEITLD
NOVEKCEKTECEYFIASVTVIYKYKTYVAKINTSEITLGTFLINLSPENIDPRV
IELYSRAEKRLSGSVFDEIEMREYNTYTORLAGREDEDINTIDNRRLADSEIV
ADLGVNGRYVAVASVITLESISVGEINFKSPFGMLMVLIVAAVLIVFALNR
TNIAIQADIRMYIPIDIMKQSGGVSDQININILAGHOLQOEERRLDEQORSA
LEFRASDGIKREFRGYKPLENEAGEYEMSK"
14122..17166
/note="ORF 9: similar to Kaposi's sarcoma-associated
herpesvirus ORF 9"
/codon_start=1
/product="DNA polymerase"
/protein_id="AAd21336.1"
/db_xref="GI:4494914"

CDS

/translation="MDFPNYLGPRGPRPHSGRTDAPAPAGAGVOPPPYCRILPA
CIRTPAGAGMIEVITIPPPYTFENKARDVLLANRSWMTADKRPVAPDPDOSITF
HAYDVETTYADRCAEVSPRODIIISGVYKILGTEDEGTSVCAVNFQOYGYFA
KVPAGIVNTYILQOALKNTAGAACGFESTRNKRNLKTYDVAEHPVEITLSSGML
STLSRLVACGEVFNESVNDVAFRFLDHGFTLFCWYSCARATIDALADATLAFD
CSMEDLSVADBSQMDPARYAVDFIECHGEGFAPCPDAGVAVIOISCVFTTRGAP
NPNILTSVGTCDPIPPDVLDEPSEYHMLYSFPMIIDEVDFITGINISFDPLY
ITRASQVNLINREYTKIKTGSIFEVHEPGRGGGFSMSVSKITAGIYVPIDMTOCR
EKLISLDKILDTVAROCGCKEDVSYDIPPLFGSGGGRKAGSYCVMSVLMVL
LKMEIIVHEISIAKLAKIOARVYLTDOQLVFECLLEAAARENFIIPVTPREGOG
YOGATVINDIGEFYDPEVLVDFALYSISOAHNLGYSTMHGRDHLHP/LPPDDY
ETVYSGPVHVGKHKRRESILGRLITVYLEKRRARIIRRTAACODPSLTLIDKOLA
IKVTCNAVYGTGVAAGILPCINTAIEYTLKRTMLEKSKSYEALITTEDLTKRGRE
VYARGAFRRVYVYGTDSLFIACDGYSAEAVSAFCDLDAARTADLPFPKILEKKT
FLCILLRLKRRKRIGLVLDKWMKVVADIRKTACFVDECRALIDVLHPDEVKAA
RILCKLRPHVYEEGLPAGFKIYEVLANASYLDLNSVVPLEOLFSELSRPVCDYK
TNNLPHLAVOGLASRCELDPOVHRIRIYVFDVADGSKSDAEHPDVYVROHQIVAV
DLYEPKLVHGANILQCLPNNADOTVAIILVNLVNPVKLS"
17261..18511
/note="ORF 10: similar to Kaposi's sarcoma-associated
herpesvirus ORF 10"
/codon_start=1
/product="unknown"
/protein_id="AAd21337.1"
/db_xref="GI:4494915"

CDS

/translation="MLVNLVSLGDMWETFRGRFSVNLTRIQTEFGHGAYARVL
PESLDOLHOFARFGLVRLKLELPEFSQVALLVPLDGGADADAARVAGVLLDSRP
LTVWVNASGRHTIRCLFLPKIDLERVATVFGNGAGARGSTPKPVCANSLGPG
LRVSGEASOTSPHSVAVPTANSAACSLRLQVREPSSDAAHDAIDAPKRYVFN
SGGVNCKASVHTLSRCKTAOMETIYAPGPNMEIYVIGSGSDAPVLPHTGGRYGVNA
DAEKTIQPGSSHEVAVQILFOOGAARBDLFLVYTGAVPELVFVYTPMLLSGCTHL
RLFNNGTPTTIKRTDILVAAAAPCVVNLSSADAPADVLVSPDGLISINAFITPVG
FPGVVSACCHVSLRDNQVHERMNH"
18520..19749
/note="ORF 11: similar to Kaposi's sarcoma-associated
herpesvirus ORF 11"

CDS

Dd	3181	CGGCCAAGGCAATTGTCGCCGTTTTCACAAATTCCTAATTTGTCATCACTGCACAGATGCA	3240
Qy	3241	GTTAACTGTAAATGTCATGATGTTTATAGTTCGCACATGCACGGGTTTAAACAGAGAATATTTCA	3300
Dd	3241	GTTAACTGTAAATGTCATGATGTTTATAGTTCGCACATGCACGGGTTTAAACAGAGAATATTTCA	3300
Qy	3301	CAATTATTAACAAATTAACCCACGAGACATGTACTTAATGTAAAGTACGTAAAGTATA	3360
Dd	3301	CAATTATTAACAAATTAACCCACGAGACATGTACTTAATGTAAAGTACGTAAAGTATA	3360
Qy	3361	TAGTTAAATCAATATTCGCTTTCACATTAATGAGCAAAAACGAAAAATGTAACTGGTTAG	3420
Dd	3361	TAGTTAAATCAATATTCGCTTTCACATTAATGAGCAAAAACGAAAAATGTAACTGGTTAG	3420
Qy	3421	CCCTACCTTGTTTGGATGGATGATTTATGTTACATGTAATAAATAATATATATATTAACGTT	3480
Dd	3421	CCCTACCTTGTTTGGATGGATGATTTATGTTACATGTAATAAATAATATATATATTAACGTT	3480
Qy	3481	TTTTTACGTAAACATATTTGTAAATTTAATCAGCTGATGTTTATGTTGGCTACTAACACACA	3540
Dd	3481	TTTTTACGTAAACATATTTGTAAATTTAATCAGCTGATGTTTATGTTGGCTACTAACACACA	3540
Qy	3541	ATGTTTGGATTAAGACCATPTAATGTTAGTAGAGCTTCAACTTATATTTTATTCCAAATGT	3600
Dd	3541	ATGTTTGGATTAAGACCATPTAATGTTAGTAGAGCTTCAACTTATATTTTATTCCAAATGT	3600
Qy	3601	TTTAAAGAGCATGTGTAATATATTTTAAACGCGATTCAGAAATAGGGCAACGCTGCGCGT	3660
Dd	3601	TTTAAAGAGCATGTGTAATATATTTTAAACGCGATTCAGAAATAGGGCAACGCTGCGCGT	3660
Qy	3661	ATTAAGTGTAAACATGATGCTTTTAACTTTTCTCTGTTTATTAACAGCCCAATAGT	3720
Dd	3661	ATTAAGTGTAAACATGATGCTTTTAACTTTTCTCTGTTTATTAACAGCCCAATAGT	3720
Qy	3721	TACGTCACACGTGAGTAAACGTAAACCTCCACATTCACAGGAATACGGGTCAAGCT	3780
Dd	3721	TACGTCACACGTGAGTAAACGTAAACCTCCACATTCACAGGAATACGGGTCAAGCT	3780
Qy	3781	AACACAGAAAAAGGACTTATATAGTGTGGAGAAACAGCTGAAATTAATTTGTCTGCTGGT	3840
Dd	3781	AACACAGAAAAAGGACTTATATAGTGTGGAGAAACAGCTGAAATTAATTTGTCTGCTGGT	3840
Qy	3841	TATGTTACAAATACAAAAATTAATACAACAGATGTTTACAAAATGGTAGCTGGTCAACA	3900
Dd	3841	TATGTTACAAATACAAAAATTAATACAACAGATGTTTACAAAATGGTAGCTGGTCAACA	3900
Qy	3901	CCAAATTTTCCATGGGACAGAAAAAGATGTCACACCTGCTGATGCTCTAAATGGACCC	3960
Dd	3901	CCAAATTTTCCATGGGACAGAAAAAGATGTCACACCTGCTGATGCTCTAAATGGACCC	3960
Qy	3961	GTGCACATTCACGGGGAGATATAGTCCTTAAATTTGGATCCAAATTTCTATGAGGT	4020
Dd	3961	GTGCACATTCACGGGGAGATATAGTCCTTAAATTTGGATCCAAATTTCTATGAGGT	4020
Qy	4021	AATGAAGGTATGATTTAATTTGTAAGTAATGTCGTTTTGTATTTTCAAGACACAGAA	4080
Dd	4021	AATGAAGGTATGATTTAATTTGTAAGTAATGTCGTTTTGTATTTTCAAGACACAGAA	4080
Qy	4081	AACGTAAATGCGGANTCAATGAACCACTCTGTGAATTCGAAATGTATTTAAACCCACG	4140
Dd	4081	AACGTAAATGCGGANTCAATGAACCACTCTGTGAATTCGAAATGTATTTAAACCCACG	4140
Qy	4141	GCAGTGAACATGGGAGTACCTACCTACCAACATGTTTATTAACATAAGAGATGCAATY	4200
Dd	4141	GCAGTGAACATGGGAGTACCTACCTACCAACATGTTTATTAACATAAGAGATGCAATY	4200
Qy	4201	ACATTTAAATGTCTATTTGCTATACACTGCTGGATCAACACATTAAGTAGACGTCGA	4260
Dd	4201	ACATTTAAATGTCTATTTGCTATACACTGCTGGATCAACACATTAAGTAGACGTCGA	4260
Qy	4261	AACAAAAAGTGTCAAACTCTTTCCCAACGCTTTAATGCTGCTGATGTGAAAGTCCACAA	4320
Dd	4261	AACAAAAAGTGTCAAACTCTTTCCCAACGCTTTAATGCTGCTGATGTGAAAGTCCACAA	4320

QY 4321 ATAGACAATGGGTACATAGACATTTGGCTTGTCCAGAAATACAAACCATGACATCAATT 4380
|||
Db 4321 ATAGACAATGGGTACATAGACATTTGGCTTGTCCAGAAATACAAACCATGACATCAATT 4380
QY 4381 ACTGTAAAGTGTAGCGAGCGGTACACATTTGGGGCTGAAGCATTTAAAGTGCACAAAC 4440
|||
Db 4381 ACTGTAAAGTGTAGCGAGCGGTACACATTTGGGGCTGAAGCATTTAAAGTGCACAAAC 4440
QY 4441 ACAACTTGGGTCCACCATTTACCTAAGTGTATTAGTACAAATTAACCCAGACACACC 4500
|||
Db 4441 ACAACTTGGGTCCACCATTTACCTAAGTGTATTAGTACAAATTAACCCAGACACACC 4500
QY 4501 ATGCGAAGAAACACCCATGCGCAGAAACACCCAGCCAGATTATCAAAAATTAATTTGCA 4560
|||
Db 4501 ATGCGAAGAAACACCCATGCGCAGAAACACCCAGCCAGATTATCAAAAATTAATTTGCA 4560
QY 4561 ACCGCTAAACCTGCACACACAAATGCGTTTGTACAACTGTTTCTCCAGAGAA 4620
|||
Db 4561 ACCGCTAAACCTGCACACACAAATGCGTTTGTACAACTGTTTCTCCAGAGAA 4620
QY 4621 GACGACGTTACTTGTGTAAAGCCATTTTGAAGGATTCAATGTAAAGGCTGAAGATGAC 4680
|||
Db 4621 GACGACGTTACTTGTGTAAAGCCATTTTGAAGGATTCAATGTAAAGGCTGAAGATGAC 4680
QY 4681 AAGGAAAAATACAGTGTGTGCGAGCGTTGAGCTAATATGTGACACGAGATTACTTAA 4740
|||
Db 4681 AAGGAAAAATACAGTGTGTGCGAGCGTTGAGCTAATATGTGACACGAGATTACTTAA 4740
QY 4741 ATGCACTCTACAGTTTCTGTGTAATGTTGTCCAAAGGAAACATGAGCTCTCAAAATGCC 4800
|||
Db 4741 ATGCACTCTACAGTTTCTGTGTAATGTTGTCCAAAGGAAACATGAGCTCTCAAAATGCC 4800
QY 4801 AAGTGTCTAGAAAAAATGTCACAAACCCCTCAAGACCTTTAAACGGAGATATATAGT 4860
|||
Db 4801 AAGTGTCTAGAAAAAATGTCACAAACCCCTCAAGACCTTTAAACGGAGATATATAGT 4860
QY 4861 ACAAGCGAAGAGATGCTTTTAAAGTACGAAACAATATATATTAATGTAAATGAAGAGT 4920
|||
Db 4861 ACAAGCGAAGAGATGCTTTTAAAGTACGAAACAATATATATTAATGTAAATGAAGAGT 4920
QY 4921 TATCAACTTTTAAAGAGATGATGCGGATTTGTATGCTTAAAGACGATTTAAAAACAGTT 4980
|||
Db 4921 TATCAACTTTTAAAGAGATGATGCGGATTTGTATGCTTAAAGACGATTTAAAAACAGTT 4980
QY 4981 GACTGGGAGCCAAAAGCGCTATATGTGATTTGAAAAATGTAAAGCCACGCCCAAAATT 5040
|||
Db 4981 GACTGGGAGCCAAAAGCGCTATATGTGATTTGAAAAATGTAAAGCCACGCCCAAAATT 5040
QY 5041 ACAAGCGAAGAAATACATCGCGTGAAGAGCTTTTATCGATTTTGGACACCGCTAAACATTT 5100
|||
Db 5041 ACAAGCGAAGAAATACATCGCGTGAAGAGCTTTTATCGATTTTGGACACCGCTAAACATTT 5100
QY 5101 TCGTGCATTCGTGACTTTTCTTATGTTAGTGAAGATGAATGACACGATGATTAAGTAATACG 5160
|||
Db 5101 TCGTGCATTCGTGACTTTTCTTATGTTAGTGAAGATGAATGACACGATGATTAAGTAATACG 5160
QY 5161 TGGAAATTAACCGTTTCCAAAGTGTGAACAAATCACTTGCACGCGCTCAAAATTTGCAAC 5220
|||
Db 5161 TGGAAATTAACCGTTTCCAAAGTGTGAACAAATCACTTGCACGCGCTCAAAATTTGCAAC 5220
QY 5221 GGAAGAGCTGTAACAGGTTCTTCAAGGTTTCAAAATTCGGTCAATCTGTTAACCATTTGGT 5280
|||
Db 5221 GGAAGAGCTGTAACAGGTTCTTCAAGGTTTCAAAATTCGGTCAATCTGTTAACCATTTGGT 5280
QY 5281 TGTGAATCTGATTTACTCTAATTTGGCAGTGAATTTCTACATGGAAGATTTCAATCGTGG 5340
|||
Db 5281 TGTGAATCTGATTTACTCTAATTTGGCAGTGAATTTCTACATGGAAGATTTCAATCGTGG 5340
QY 5341 GATCAGCAGACTTCTAGCTGCGTGCAGCTGTTTCAATGCTTCTGACACACCTTAACCA 5400
|||
Db 5341 GATCAGCAGACTTCTAGCTGCGTGCAGCTGTTTCAATGCTTCTGACACACCTTAACCA 5400

QY 5401 GAAACCAAAAAACCAACACGCGCAAGCGCAGAGACACCACCAACCAACCCCAAAAGTT 5460
|||
Db 5401 GAAACCAAAAAACCAACACGCGCGCAAGCGCAGAGACACCACCAACCAACCCCAAAAGTT 5460
QY 5461 GGAACACATACACCATTTCAAAACACACACCAACAAATCCACCAATAGACACCCCAATGAGT 5520
|||
Db 5461 GGAACACATACACCATTTCAAAACACACACCAACAAATCCACCAATAGACACCCCAATGAGT 5520
QY 5521 AAATGGAAGGCAATGCGTGTAGTCTTTTCCAAAGTGTGCGGCTCTGTTAATGCTA 5580
|||
Db 5521 AAATGGAAGGCAATGCGTGTAGTCTTTTCCAAAGTGTGCGGCTCTGTTAATGCTA 5580
QY 5581 CTTCGCTCCCTTTATTTGTTTCTTAAATACGTGTTTGTCTTCAGCAGGTTGCGC 5640
|||
Db 5581 CTTCGCTCCCTTTATTTGTTTCTTAAATACGTGTTTGTCTTCAGCAGGTTGCGC 5640
QY 5641 AGGCAAACTGCGCAGCATTAACCAATCTGCCAACCGCGCTGATTCGGAAATTAAGTTTA 5700
|||
Db 5641 AGGCAAACTGCGCAGCATTAACCAATCTGCCAACCGCGCTGATTCGGAAATTAAGTTTA 5700
QY 5701 CATTTATCAAGGTTGCCAATTAAGTGGTTTAAATATCTAATTTGGTTCATTTGTTT 5760
|||
Db 5701 CATTTATCAAGGTTGCCAATTAAGTGGTTTAAATATCTAATTTGGTTCATTTGTTT 5760
QY 5761 ATGTTGACCCGTTTATAGTTATTCGCGCACCTTGTGGCTACATTAATAGCAGCATCACT 5820
|||
Db 5761 ATGTTGACCCGTTTATAGTTATTCGCGCACCTTGTGGCTACATTAATAGCAGCATCACT 5820
QY 5821 TTCCAGCTTATATCTTACGTAATGACATCATACGCTTAACGTCACGTGGCGTGCAT 5880
|||
Db 5821 TTCCAGCTTATATCTTACGTAATGACATCATACGCTTAACGTCACGTGGCGTGCAT 5880
QY 5881 TGTGGCGGGCGCTGAAAAATACAAAGGGGTACATTAATCCATTCAGGGCGGACATTAAG 5940
|||
Db 5881 TGTGGCGGGCGCTGAAAAATACAAAGGGGTACATTAATCCATTCAGGGCGGACATTAAG 5940
QY 5941 ACACGTTTATTAACATATATCGATGCGCCAAACATCTGTCGTAGCAGACTGATA 6000
|||
Db 5941 ACACGTTTATTAACATATATCGATGCGCCAAACATCTGTCGTAGCAGACTGATA 6000
QY 6001 GAAAAACATTTTAAAGTTTGTGTAAGCAATGTAATACATTAATGGCTTCCAAAGGCA 6060
|||
Db 6001 GAAAAACATTTTAAAGTTTGTGTAAGCAATGTAATACATTAATGGCTTCCAAAGGCA 6060
QY 6061 ACGCGGAGCAACCCCTGGAAGATATATCAGGGGTCTCGGCCCGATAGGTGCGTGGAT 6120
|||
Db 6061 ACGCGGAGCAACCCCTGGAAGATATATCAGGGGTCTCGGCCCGATAGGTGCGTGGAT 6120
QY 6121 ACGTGTACGCGTATTCGAACAAAGACTTCCCTTTCGCGAGGCGTCACTCGGCAACA 6180
|||
Db 6121 ACGTGTACGCGTATTCGAACAAAGACTTCCCTTTCGCGAGGCGTCACTCGGCAACA 6180
QY 6181 GACCATCTGATCTGGGCTTTCTCGCTTACCAATCTTTACGACTTACAGTGAACAG 6240
|||
Db 6181 GACCATCTGATCTGGGCTTTCTCGCTTACCAATCTTTACGACTTACAGTGAACAG 6240
QY 6241 AATTCCTCTACCGCTAAACCCCGATCAAAAAAGTTGAACACACGACGCGCTCCGCTTA 6300
|||
Db 6241 AATTCCTCTACCGCTAAACCCCGATCAAAAAAGTTGAACACACGACGCGCTCCGCTTA 6300
QY 6301 AGGTGACGTCGCTTTCACAGAGAGTTATGTTTCAACAAATGAAGTTTATTCAGGCGCG 6360
|||
Db 6301 AGGTGACGTCGCTTTCACAGAGAGTTATGTTTCAACAAATGAAGTTTATTCAGGCGCG 6360
QY 6361 TGTGTAACGTTACCGGCTTAAAGCAATATCGAGGAAGCAGGCGCTCTTCTTGGGTACA 6420
|||
Db 6361 TGTGTAACGTTACCGGCTTAAAGCAATATCGAGGAAGCAGGCGCTCTTCTTGGGTACA 6420
QY 6421 CGCAGTTATATGAACCGGGTCCACCTCAGACATATGGAACCCCTCTGGAATGTCGCGAGT 6480
|||
Db 6421 CGCAGTTATATGAACCGGGTCCACCTCAGACATATGGAACCCCTCTGGAATGTCGCGAGT 6480
QY 6481 TACCGGACAAAGATGAGATGTTCTGTGGCGTTGTTGTTACGGAAGGTTTAAAGAAAGAC 6540

Db 6481 TACCGGCAAGATGAGATGTTCTTGCGCTTGTTGTAGGAAAGGTTTAAAGAAAGAC 6540
 QY 6541 TGTGAGAGGGCTGTCTGTCGCCGGGTGTTCCAGACCCAGAGGTGCAGATTGCCGGAC 6600
 Db 6541 TGTGAGAGGGCTGTCTGTCGCCGGGTGTTCCAGACCCAGAGGTGCAGATTGCCGGAC 6600
 QY 6601 GCCAGGCTTTAAAGTCCGTTGTAGCAGCAAGACCTGTTTGCACCTCAGCGTCAAGAA 6660
 Db 6601 GCCAGGCTTTAAAGTCCGTTGTAGCAGCAAGACCTGTTTGCACCTCAGCGTCAAGAA 6660
 QY 6661 TGGCAAGGTTTAAAGTCCGTTGTAGCAGCAAGACCTGTTTGCACCTCAGCGTCAAGAA 6720
 Db 6661 TGGCAAGGTTTAAAGTCCGTTGTAGCAGCAAGACCTGTTTGCACCTCAGCGTCAAGAA 6720
 QY 6721 TCGCCAGGCTTGAAGTCCGTTGTAGCAGCAAGACCTGTTTGCACCTCAGCGTCAAGAA 6780
 Db 6721 TCGCCAGGCTTGAAGTCCGTTGTAGCAGCAAGACCTGTTTGCACCTCAGCGTCAAGAA 6780
 QY 6781 TCAATGAGAGCACTTACAAAATTGCCAAGATAGTGCAGCAAAAAGTTTCAACGACGC 6840
 Db 6841 TCGCGAAAAGCAGAGAGGCTGCTCCACATGATGTGTGACACGCTGTCGCCGAGCTCG 6900
 QY 6841 TCGCGAAAAGCAGAGAGGCTGCTCCACATGATGTGTGACACGCTGTCGCCGAGCTCG 6900
 Db 6901 CCTTGAATGAGGCTGATGTTCTGAGAGTGTCCAGAGAGGCTGAGATTCCTGACACT 6960
 QY 6901 CCTTGAATGAGGCTGATGTTCTGAGAGTGTCCAGAGAGGCTGAGATTCCTGACACT 6960
 Db 6961 ACATATGCTGCGCCATATTTGATGTGTGTACTACACAGAGGCTAGGGTTTAAAGCGCTTAG 7020
 QY 6961 ACATATGCTGCGCCATATTTGATGTGTGTACTACACAGAGGCTAGGGTTTAAAGCGCTTAG 7020
 Db 7021 AGCGGCTGCGGCGGCAAGGCGCTTACAGTGGGCGTCAAGTTCGCTGCCAATTGCG 7080
 QY 7021 AGCGGCTGCGGCGGCAAGGCGCTTACAGTGGGCGTCAAGTTCGCTGCCAATTGCG 7080
 Db 7021 AGCGGCTGCGGCGGCAAGGCGCTTACAGTGGGCGTCAAGTTCGCTGCCAATTGCG 7080
 QY 7081 TGGCTGACCTAACTAAAGTGCAGAGAGCAGCGCCAGGGGCAAAAAGGAGAGAGTAAACG 7140
 Db 7081 TGGCTGACCTAACTAAAGTGCAGAGAGCAGCGCCAGGGGCAAAAAGGAGAGAGTAAACG 7140
 QY 7141 TGTACAACTCTCTTTCTCTCCAAACAGAGAGTGGGGTTTAAATGAGGCCAGCATCAAG 7200
 Db 7141 TGTACAACTCTCTTTCTCTCCAAACAGAGAGTGGGGTTTAAATGAGGCCAGCATCAAG 7200
 QY 7201 AAAAGGCAAGGAGGCTTAAAGGGGTACCCCTCAACGCGCTGATGGTCTTCTGTTCA 7260
 Db 7201 AAAAGGCAAGGAGGCTTAAAGGGGTACCCCTCAACGCGCTGATGGTCTTCTGTTCA 7260
 QY 7261 CGCGGTATACCTGCGGCTTACGCGGCTTCTGCGCCCACTGCTGCGCAATGATGTT 7320
 Db 7261 CGCGGTATACCTGCGGCTTACGCGGCTTCTGCGCCCACTGCTGCGCAATGATGTT 7320
 QY 7321 ATTACATGCAAGTCTTGTGCAACACCAAAAAGCTCCACGAAACGCGGTTTAAATGATGTC 7380
 Db 7321 ATTACATGCAAGTCTTGTGCAACACCAAAAAGCTCCACGAAACGCGGTTTAAATGATGTC 7380
 QY 7381 ATTATATGCGACACGCGGCAACTGAGAGTGTGACGCGTATGTCAGCGGCAACGCGG 7440
 Db 7381 ATTATATGCGACACGCGGCAACTGAGAGTGTGACGCGTATGTCAGCGGCAACGCGG 7440
 QY 7441 CAACGTGCTCAACACGCTGTTCTATAGATGTAAGATAGTTCGCCGCGTAACACCC 7500
 Db 7441 CAACGTGCTCAACACGCTGTTCTATAGATGTAAGATAGTTCGCCGCGTAACACCC 7500
 QY 7501 CTCAGGCGAGGAGCCCTTACGTGTGTACCGGAAACCGGAGCCTTTAAGACACTGAGAG 7560
 Db 7501 CTCAGGCGAGGAGCCCTTACGTGTGTACCGGAAACCGGAGCCTTTAAGACACTGAGAG 7560
 QY 7561 TTCTGGCAACTTCGCGAGCTTTAGAGACCGGCAAGAGACGAAACCGGCGGAGAGAGC 7620
 Db 7561 TTCTGGCAACTTCGCGAGCTTTAGAGACCGGCAAGAGAGACGAAACCGGCGGAGAGAGC 7620

Db 7621 TTCTGGCAACTTCGCGAGCTTTAGAGACCGGCAAGAGAGACGAAACCGGCGGAGAGC 7680
 QY 7621 ACCCAAAAGTACAGTACTGACAGTATGTGACAGCCGTAAGAGAAAGCTATCCGGATTG 7680
 Db 7621 ACCCAAAAGTACAGTACTGACAGTATGTGACAGCCGTAAGAGAAAGCTATCCGGATTG 7680
 QY 7681 GAATCAACGAGAACAGATTAATCAGTGAACCTCATCACCAACATCCAAAAGTTTCTCA 7740
 Db 7681 GAATCAACGAGAACAGATTAATCAGTGAACCTCATCACCAACATCCAAAAGTTTCTCA 7740
 QY 7741 GGGTGTTCAGAGGATTCAGTCAATGTTGGACGGAGAGGTCATGAAGTTCGTTAATTCGA 7800
 Db 7741 GGGTGTTCAGAGGATTCAGTCAATGTTGGACGGAGAGGTCATGAAGTTCGTTAATTCGA 7800
 QY 7801 TGAATTAATAAATTAATTAATTTCCGGAGACGCTCAATGCGTCAATCATCACTCAGT 7860
 Db 7801 TGAATTAATAAATTAATTAATTTCCGGAGACGCTCAATGCGTCAATCATCACTCAGT 7860
 QY 7861 TGTATTAATAAATTAATTAATTTCCGGAGACGCTCAATGCGTCAATCATCACTCAGT 7920
 Db 7861 TGTATTAATAAATTAATTAATTTCCGGAGACGCTCAATGCGTCAATCATCACTCAGT 7920
 QY 7921 TGTGTGCAACGCTGTATTGGCAGGCGCCGCGGCTGTTCTGAAATCTGTACTACAAAT 7980
 Db 7921 TGTGTGCAACGCTGTATTGGCAGGCGCCGCGGCTGTTCTGAAATCTGTACTACAAAT 7980
 QY 7981 ATCCGCGATATGAGCATCTCCCTCCGAGTGGCTAAAGATGCAATTTTACAGACCTTGTGA 8040
 Db 7981 ATCCGCGATATGAGCATCTCCCTCCGAGTGGCTAAAGATGCAATTTTACAGACCTTGTGA 8040
 QY 8041 CGAATCTTAAAGCGGCGTGTCTGACCGCGGGTCTCTACGGGCTCGAATCTGAATATCG 8100
 Db 8041 CGAATCTTAAAGCGGCGTGTCTGACCGCGGGTCTCTACGGGCTCGAATCTGAATATCG 8100
 QY 8101 TACACCGGGAGCATGTTCTGCACTTCTGTGACACACGAGCGGGGTCAACGGCTTATG 8160
 Db 8101 TACACCGGGAGCATGTTCTGCACTTCTGTGACACACGAGCGGGGTCAACGGCTTATG 8160
 QY 8161 CCCCTTTAAATATGACAGTTAGATAGACCCGAGCCTGATGATGTCCTTCCGAAATCAATTA 8220
 Db 8161 CCCCTTTAAATATGACAGTTAGATAGACCCGAGCCTGATGATGTCCTTCCGAAATCAATTA 8220
 QY 8221 AAATTAATAAATATGATATTTTCCCAACACCGCGGGATTCGAGGGGTGCACTGCGGGT 8280
 Db 8221 AAATTAATAAATATGATATTTTCCCAACACCGCGGGATTCGAGGGGTGCACTGCGGGT 8280
 QY 8281 TCGTCAAAACGAGGAGAACCCAGGAGACCTTACGTGTGCGGACCGTACATGAATTTTC 8340
 Db 8281 TCGTCAAAACGAGGAGAACCCAGGAGACCTTACGTGTGCGGACCGTACATGAATTTTC 8340
 QY 8341 TCAACTGCTGCATCGCGGCTGTTCCCGACACCAAGACCGCGGCTGTACTGTGGC 8400
 Db 8341 TCAACTGCTGCATCGCGGCTGTTCCCGACACCAAGACCGCGGCTGTACTGTGGC 8400
 QY 8401 ACAAGATCTCCGACCAACCAAAACCCAGTTCGAAACGTCGCGGACGAGACACTGG 8460
 Db 8401 ACAAGATCTCCGACCAACCAAAACCCAGTTCGAAACGTCGCGGACGAGACACTGG 8460
 QY 8461 CGGAGCTGTGTGCTGCTAAAGACCAACAGCCTCGCTTCGAGAAAGCAAGCTCTGG 8520
 Db 8461 CGGAGCTGTGTGCTGCTAAAGACCAACAGCCTCGCTTCGAGAAAGCAAGCTCTGG 8520
 QY 8521 ACCTGTTCCGGAATTCATCATGTCTGTACGCGAGATCAAACTGAACGGGGCATTTCTAA 8580
 Db 8521 ACCTGTTCCGGAATTCATCATGTCTGTGTACGCGAGATCAAACTGAACGGGGCATTTCTAA 8580
 QY 8581 GGGCATGTGGCCAGATTCAGTTCTGTACGCAAGCTGTGACGCTCTACGCGGGTGTAC 8640
 Db 8581 GGGCATGTGGCCAGATTCAGTTCTGTGTACGCAAGCTGTGACGCTCTACGCGGGTGTAC 8640
 QY 8641 AGACGATGATGCGGAGAAATACCCGAGTGTGGGCTCGCGGCAATCGCACACCGG 8700
 Db 8641 AGACGATGATGCGGAGAAATACCCGAGTGTGGGCTCGCGGCAATCGCACACCGG 8700

QY	8701	TGCGTAACTTGCGCAGAAATATACGCGCGCACCGCCCTCACCGCTCCAGACGACGGCGCTC	8760
Db	8701	TGGCTTACCTGCGCAGAAATATACGCGCGCACCGCCCTCACCGCTCCAGACGACGGCGCTC	8760
QY	8761	AGCGGTCGCGCGCACAGGGCGCGCTGGCTCCCGTGATTAACGCTTCCCATGGTATCTCAACA	8820
Db	8761	AGCGGTCGCGCGCACAGGGCGCGCTGGCTCCCGTGATTAACGCTTCCCATGGTATCTCAACA	8820
QY	8821	AATACACGGGGGCTACACGGGAAACAACAAGTTTTTCCACTGGCGGAACCTGGGGTACTTCG	8880
Db	8821	AATACACGGGGGCTACACGGGAAACAACAAGTTTTTCCACTGGCGGAACCTGGGGTACTTCG	8880
QY	8881	CGGGGCGCGCGCTGAGACCGCAACTGTGTGGCGGAAAGCTCCCTTTAAGAAAAGGGCG	8940
Db	8881	CGGGGCGCGCGGCTGAGACCGCAACTGTGTGGCGGAAAGCTCCCTTTAAGAAAAGGGCG	8940
QY	8941	TCACGGCCATCTTAAGAAAGAGACACGTCATGATGACCCCCCATTTATGACCGCCATAATTA	9000
Db	8941	TCACGGCCATCTTAAGAAAGAGACACGTCATGATGACCCCCCATTTATGACCGCCATAATTA	9000
QY	9001	AGCAGCGCGCGGACAGACAATCAGCAGCTTCGAGGGGAAAGGCTTAAAGAGAGCGCTGC	9060
Db	9001	AGCAGCGCGCGGACAGACAATCAGCAGCTTCGAGGGGAAAGGCTTAAAGAGAGCGCTGC	9060
QY	9061	AGGGGCTGTAGAGATTAAGGACAACCTAACATTAATGAAGTGGGTAACTGTGAGCTTA	9120
Db	9061	AGGGGCTGTAGAGATTAAGGACAACCTAACATTAATGAAGTGGGTAACTGTGAGCTTA	9120
QY	9121	TACGACACCTGGGGAAAGGGCTGCCAGAGACTTAACCTCCGAGAGCTGCATATTACCTCG	9180
Db	9121	TACGACACCTGGGGAAAGGGCTGCCAGAGACTTAACCTCCGAGAGCTGCATATTACCTCG	9180
QY	9181	GTGACTATTGTATGTGTGACGGACGAGGTTTTATTAGCTTGGATTAATATGACACAGTCAG	9240
Db	9181	GTGACTATTGTATGTGTGACGGACGAGGTTTTATTAGCTTGGATTAATATGACACAGTCAG	9240
QY	9241	GCGTGCCGTGAGACTATCGAGAGACCGGGTGCCCTTAATAGAGATCGCGACGAGCAACG	9300
Db	9241	GCGTGCCGTGAGACTATCGAGAGACCGGGTGCCCTTAATAGAGATCGCGACGAGCAACG	9300
QY	9301	ATCTTCACTGTGTAGACAGCAGCATATTCGCACCGCTTCTGTACGGCCCCCAGAGAAC	9360
Db	9301	ATCTTCACTGTGTAGACAGCAGCATATTCGCACCGCTTCTGTACGGCCCCCAGAGAAC	9360
QY	9361	AGCTACCGACCCCTTAGCGCGCGGCCCTACTGTGGCGGGAAACAAGCAAAATTTAACGGCG	9420
Db	9361	AGCTACCGACCCCTTAGCGCGCGGCCCTACTGTGGCGGGAAACAAGCAAAATTTAACGGCG	9420
QY	9421	TGCTGAGGATCTAGACCTTTAGGAAAACGTGGCAGGGCGGCAACAATGGCCAGGGAAC	9480
Db	9421	TGCTGAGGATCTAGACCTTTAGGAAAACGTGGCAGGGCGGCAACAATGGCCAGGGAAC	9480
QY	9481	TCGGAGCACTTAAGCGCGAGCTGTGTGGCCCTCGCGCTGACTTGAAGTGTGGTTATCTTGG	9540
Db	9481	TCGGAGCACTTAAGCGCGAGCTGTGTGGCCCTCGCGCTGACTTGAAGTGTGGTTATCTTGG	9540
QY	9541	CGGACCCCGCAAGTATCGACGCTGCCCGCATTTCAAAAACAAAAACACAGATTAAGAAC	9600
Db	9541	CGGACCCCGCAAGTATCGACGCTGCCCGCATTTCAAAAACAAAAACACAGATTAAGAAC	9600
QY	9601	TGAACCGGACCTTCTGCGCGTCTAGCGCAACAACTCGGTAGAGACGTCAGCGCTGT	9660
Db	9601	TGAACCGGACCTTCTGCGCGTCTAGCGCAACAACTCGGTAGAGACGTCAGCGCTGT	9660
QY	9661	CGCTGCAAGTGGACACCTTGCGCAAAAAACATCGAGAACAACTGGGCGAGCTGGAGCGCA	9720
Db	9661	CGCTGCAAGTGGAGCACTTGCGCAAAAAACATCGAGAACAACTGGGCGAGCTGGAGCGCA	9720
QY	9721	GTCGTGGCAGAGATTTAGACCGGAGAGCAATTTTGAACAATACCTGAGACCGCGAT	9780
Db	9721	GTCGTGGCAGAGATTTAGACCGGAGAGCAATTTTGAACAATACCTGAGACCGCGAT	9780

QY	9781	GTCACTATCACTACGCGTTACTTTTATAGTTTACGCGGGCGGGTTAATAGATGTAAACA	9840
Db	9781	GTCACTATCACTACGCGTTACTTTTATAGTTTACGCGGGCGGGTTAATAGATGTAAACA	9840
QY	9841	TGTGCGTAATTAAGATGTGAAGTGTGTAAAGAGTACAGGAGGTGTATTTATTTGCA	9900
Db	9841	TGTGCGTAATTAAGATGTGAAGTGTGTAAAGAGTACAGGAGGTGTATTTATTTGCA	9900
QY	9901	TCGGTGCAAAGAAAGCTCTGTCCGGATTGAAACCGGGCTTGAGGTTTCTGTCAACACTGC	9960
Db	9901	TCGGTGCAAAGAAAGCTCTGTCCGGATTGAAACCGGGCTTGAGGTTTCTGTCAACACTGC	9960
QY	9961	GGGGTATCTCCCGGATCCCGACCCAGACTTATACGTACGTACGTGCTTGCTGTACAGT	10020
Db	9961	GGGGTATCTCCCGGATCCCGACCCAGACTTATACGTACGTACGTGCTTGCTGTACAGT	10020
QY	10021	GCCAGAGGGAATGGAAGTGTGTCCAAATGAGGGGTCCAGTTTACGCGGGGTGTGGCAG	10080
Db	10021	GCCAGAGGGAATGGAAGTGTGTCCAAATGAGGGGTCCAGTTTACGCGGGGTGTGGCAG	10080
QY	10081	ACCCAGACTGCGATCACCTCTGTAAAGAGTTAGGGCGAGCCAAATACAGGCGCTTTTG	10140
Db	10081	ACCCAGACTGCGATCACCTCTGTAAAGAGTTAGGGCGAGCCAAATACAGGCGCTTTTG	10140
QY	10141	AGACAGAACTGAGCCAGCTGGGTCTAAAGTTAAACAAAAGTTTCGAGCCGACGACGACG	10200
Db	10141	AGACAGAACTGAGCCAGCTGGGTCTAAAGTTAAACAAAAGTTTCGAGCCGACGACGACG	10200
QY	10201	GCGTCCGGTCTCTGCAAGATCAGTTAAGGAGTCTGCTGGCGGCCATTCAGAGATCACA	10260
Db	10201	GCGTCCGGTCTCTGCAAGATCAGTTAAGGAGTCTGCTGGCGGCCATTCAGAGATCACA	10260
QY	10261	ATTATATTCAAAGGGGTGTCCGCGTCATTCATGGAATCATCAATCTAATTTATTTGGACG	10320
Db	10261	ATTATATTCAAAGGGGTGTCCGCGTCATTCATGGAATCATCAATCTAATTTATTTGGACG	10320
QY	10321	CCGGGCAAAACGGCGCTCCAGACCGGGGACCGAAAAAGAGTCTCACAATGGCCAGACTGC	10380
Db	10321	CCGGGCAAAACGGCGCTCCAGACCGGGGACCGAAAAAGAGTCTCACAATGGCCAGACTGC	10380
QY	10381	TAAACACAGAGGCCGATATGACAGAGACCGGTGCGCTAATTAACCCCAACTTAAGGCGCA	10440
Db	10381	TAAACACAGAGGCCGATATGACAGAGACCGGTGCGCTAATTAACCCCAACTTAAGGCGCA	10440
QY	10441	CTCACTTCTAGCACTGTTTCCGACCGGATCCCATAGAAATCCGTCTGGGGGCGTCTTT	10500
Db	10441	CTCACTTCTAGCACTGTTTCCGACCGGATCCCATAGAAATCCGTCTGGGGGCGTCTTT	10500
QY	10501	TTAACTCTATAGACAGACCATAAACGCACTGAGCCGGGATTCCTCCGTGACCTTCTTC	10560
Db	10501	TTAACTCTATAGACAGACCATAAACGCACTGAGCCGGGATTCCTCCGTGACCTTCTTC	10560
QY	10561	AACAGGCAACTATACCAAGTTATGGGAAAAACAAACGAGCTGTTCACAGACTCAATA	10620
Db	10561	AACAGGCAACTATACCAAGTTATGGGAAAAACAAACGAGCTGTTCACAGACTCAATA	10620
QY	10621	GCATCTGTCGTCAGGGGAGCGCGGATCCGCAAAAACCGCCACCCCTCGAGGCCAGCA	10680
Db	10621	GCATCTGTCGTCAGGGGAGCGCGGATCCGCAAAAACCGCCACCCCTCGAGGCCAGCA	10680
QY	10681	CCACCACCGTGGCGCAACCGCGGCAAGCAGAGCTCATCAAGAAGCAGATGCGCAAG	10740
Db	10681	CCACCACCGTGGCGCAACCGCGGCAAGCAGAGCTCATCAAGAAGCAGATGCGCAAG	10740
QY	10741	AACAGTACATGAAAAAGTGGCCAGGGACGGCTTTAAAAAACTTAACAGATGTCTCACA	10800
Db	10741	AACAGTACATGAAAAAGTGGCCAGGGACGGCTTTAAAAAACTTAACAGATGTCTCACA	10800
QY	10801	CGCAGAGGGCGGTTTGGCAAAAGCATCTGCAATGGCGGTATGGGGGGGGGTCGCTTAG	10860
Db	10801	CGCAGAGGGCGGTTTGGCAAAAGCATCTGCAATGGCGGTATGGGGGGGGGTCGCTTAG	10860
QY	10861	GCAGAGCGCGGTCTTTGGCAAAAGCATCTGCAATGGCGGTATGGGGGGGGGTCGCTTAG	10920
Db	10861	GCAGAGCGCGGTCTTTGGCAAAAGCATCTGCAATGGCGGTATGGGGGGGGGTCGCTTAG	10920

Db 10861 GCGAGCGTCGAGCGTGGTGAACCAATTTCTCTCAGGGGGCGCTTCGTGCGCTTCCTT 10920
QY 10921 GGGAGCGGGCTGCGCCTCGGATCAGATTTTATTCGAAAACCTCAAGATCAATTAATAACT 10980
Db 10921 GGGAGCGGGCTGCGCCTCGGATCAGATTTTATTCGAAAACCTCAAGATCAATTAATAACT 10980
QY 10981 CACTAATATTCGACGGCCCTCAGTGGCAACAGCTAGAGATTATCAGCTGCAATTTACG 11040
Db 10981 CACTAATATTCGACGGCCCTCAGTGGCAACAGCTAGAGATTATCAGCTGCAATTTACG 11040
QY 11041 GCCTGATTAACGGGCGCCCTGAGCGCGCAGAGGAGTCTCTTCCCGGCGCCCGCAAGCTCG 11100
Db 11041 GCCTGATTAACGGGCGCCCTGAGCGCGCAGAGGAGTCTCTTCCCGGCGCCCGCAAGCTCG 11100
QY 11101 CCGTGGCCCAAGTGTTCGAGGGCGCGGAGATGCTTCGATCACAAGATGCTGTGTCAG 11160
Db 11101 CCGTGGCCCAAGTGTTCGAGGGCGCGGAGATGCTTCGATCACAAGATGCTGTGTCAG 11160
QY 11161 AGATGATATGCCCCCAGATTCAACGGAAGACTGGATAGACAGACATTTATCGTTTTT 11220
Db 11161 AGATGATATGCCCCCAGATTCAACGGAAGACTGGATAGACAGACATTTATCGTTTTT 11220
QY 11221 ACCAATTCGCCGAAGGTGATCTCAACGGGTACAAAGTCCGCTGGCTTTATACGAG 11280
Db 11221 ACCAATTCGCCGAAGGTGATCTCAACGGGTACAAAGTCCGCTGGCTTTATACGAG 11280
QY 11281 AGCTGCTCTCTCGGTGGGCTTTTATATGCGACGCTGGGAAAAGACGCTGCGGATATTT 11340
Db 11281 AGCTGCTCTCTCGGTGGGCTTTTATATGCGACGCTGGGAAAAGACGCTGCGGATATTT 11340
QY 11341 CCCTAGCGGCGGAGAAACTCTCATCTCCAACTAGACGTTAAAGGCTGAGCTCGGCC 11400
Db 11341 CCCTAGCGGCGGAGAAACTCTCATCTCCAACTAGACGTTAAAGGCTGAGCTCGGCC 11400
QY 11401 TGTATCTAAGCTAGACGAGAGAGCGCGCTGCTTAATTTCTCAAAATACCGGTGGA 11460
Db 11401 TGTATCTAAGCTAGACGAGAGAGCGCGCTGCTTAATTTCTCAAAATACCGGTGGA 11460
QY 11461 TATTTAAAGACCTGTAAGCTCTTCTGTACATCAGCTGCAAGCTGTCGAGCGGCATGATG 11520
Db 11461 TATTTAAAGACCTGTAAGCTCTTCTGTACATCAGCTGCAAGCTGTCGAGCGGCATGATG 11520
QY 11521 ATAACTAAGCGAAGCGTGTCTCTCTGCGGGGTGGGTGTGATTAATCGCGATCGGACAG 11580
Db 11521 ATAACTAAGCGAAGCGTGTCTCTCTGCGGGGTGGGTGTGATTAATCGCGATCGGACAG 11580
QY 11581 ATAACTAAGCGAAGCGTGTCTCTCTGCGGGGTGGGTGTGATTAATCGCGATCGGACAG 11580
Db 11581 ATAACTAAGCGAAGCGTGTCTCTCTGCGGGGTGGGTGTGATTAATCGCGATCGGACAG 11580
QY 11581 GCGGTTGGGAAAACGTCACACACCCCAAGGGGCGCACCAACGCGCGAAGCAAGCGCG 11640
Db 11581 GCGGTTGGGAAAACGTCACACACCCCAAGGGGCGCACCAACGCGCGAAGCAAGCGCG 11640
QY 11641 GGCCTGTCGAGCGCCACACACCTCCGAGAACCCACCTAGGGCGGAGCGTTTAAAGTTGCG 11700
Db 11641 GGCCTGTCGAGCGCCACACACCTCCGAGAACCCACCTAGGGCGGAGCGTTTAAAGTTGCG 11700
QY 11701 GTGTGAGAGCGCTCGGCGCACCGCGCACTTTCAGGTTTAACCTGGAATAAAACGTGTCG 11760
Db 11701 GTGTGAGAGCGCTCGGCGCACCGCGCACTTTCAGGTTTAACCTGGAATAAAACGTGTCG 11760
QY 11761 GGCACCGAGAGACAGGACGACCAAGAGAGCATCTGATGTTTAAAAAAATATTTGTC 11820
Db 11761 GGCACCGAGAGACAGGACGACCAAGAGAGCATCTGATGTTTAAAAAAATATTTGTC 11820
QY 11821 CCGCACATCTTTAAGGTGAGAGGTATCCGCAAGGTGGCCACTCGGTGACCGTATATGA 11880
Db 11821 CCGCACATCTTTAAGGTGAGAGGTATCCGCAAGGTGGCCACTCGGTGACCGTATATGA 11880
QY 11881 GGGTGGAGCGAGACCGCGGTGACCGGCAAGCAAGAGGTATCCGACCGGTGCGGAGTAC 11940
Db 11881 GGGTGGAGCGAGACCGCGGTGACCGGCAAGCAAGAGGTATCCGACCGGTGCGGAGTAC 11940
QY 11941 GAGATCAACCAATGAGACGAGCTTACAGTGTTCAGCTCATCGGCTTAACGTCAC 12000
Db 11941 GAGATCAACCAATGAGACGAGCTTACAGTGTTCAGCTCATCGGCTTAACGTCAC 12000

Db 11941 GAGATCAACCAATGAGACGAGCTTACAGTGTTCAGCTCATCGGCTTAACGTCAC 12000
QY 12001 GGCATAGTAACACCTACACGAGGAGACTTCACTAACGAGACCGTGTTCGCAACCG 12060
Db 12001 GGCATAGTAACACCTACACGAGGAGACTTCACTAACGAGACCGTGTTCGCAACCG 12060
QY 12061 GTGAGGGGCTCAGGATTAACATCCAGCGATCTTACAGTACGCGGTGCTGTACAGACA 12120
Db 12061 GTGAGGGGCTCAGGATTAACATCCAGCGATCTTACAGTACGCGGTGCTGTACAGACA 12120
QY 12121 CCGGATGAGTTCCGGGAATTTACAGGGTCAGAACACGGTCAACGCGGATCGTGGAG 12180
Db 12121 CCGGATGAGTTCCGGGAATTTACAGGGTCAGAACACGGTCAACGCGGATCGTGGAG 12180
QY 12181 ATGATCGCGGCTTGGCGGAAACCTGATATTTTGTACACGCGCTTGGAGACAGGTA 12240
Db 12181 ATGATCGCGGCTTGGCGGAAACCTGATATTTTGTACACGCGCTTGGAGACAGGTA 12240
QY 12241 GAGGTGTCCTCCGTTCTGCGCAACAGCTACGCTCGGTGCGGAGAAAACCGAAAC 12300
Db 12241 GAGGTGTCCTCCGTTCTGCGCAACAGCTACGCTCGGTGCGGAGAAAACCGAAAC 12300
QY 12301 GGCCTGGGCGCGCGGTGCTCAAAATTAACCATGCTGAGCTTGGGACCGCGAGCC 12360
Db 12301 GGCCTGGGCGCGCGGTGCTCAAAATTAACCATGCTGAGCTTGGGACCGCGAGCC 12360
QY 12361 ACCACCGAAACGGGGCTTTCGCGACGCTGGGAGATACCGTATCGTGAAGCGGAG 12420
Db 12361 ACCACCGAAACGGGGCTTTCGCGACGCTGGGAGATACCGTATCGTGAAGCGGAG 12420
QY 12421 GACCCCAAGTCGGGCTGTGCGGCTGACGCTGTGGAACCTTCCCGAGGGCGATACAG 12480
Db 12421 GACCCCAAGTCGGGCTGTGCGGCTGACGCTGTGGAACCTTCCCGAGGGCGATACAG 12480
QY 12481 ACAGCGCAGAGGCGCGCTACCACTCTGAGGCAAGAGAGTGACGCGGACCTTACGTC 12540
Db 12481 ACAGCGCAGAGGCGCGCTACCACTCTGAGGCAAGAGAGTGACGCGGACCTTACGTC 12540
QY 12541 CCGCTCTCCAGTAACTAATTCACGGGACGTAACCTCGCTCAATGATGTTATTCAG 12600
Db 12541 CCGCTCTCCAGTAACTAATTCACGGGACGTAACCTCGCTCAATGATGTTATTCAG 12600
QY 12601 AAAACCTTAAGCGCCATCAAGAAAGCTGTCCGATACCCAGCAAAAGGATGAG 12660
Db 12601 AAAACCTTAAGCGCCATCAAGAAAGCTGTCCGATACCCAGCAAAAGGATGAG 12660
QY 12661 CAGTACTAGAAACCGAGGGGGTGTCTTCTCTGTGACACCGCTTAACGCGCTAAC 12720
Db 12661 CAGTACTAGAAACCGAGGGGGTGTCTTCTCTGTGACACCGCTTAACGCGCTAAC 12720
QY 12721 CTAGCTGAGAGATGCGGAATTTAAAGGACGACGACGACCCCGCACCAACCTCA 12780
Db 12721 CTAGCTGAGAGATGCGGAATTTAAAGGACGACGACGACCCCGCACCAACCTCA 12780
QY 12781 ACCGCGAACCGGTTTGAAAGAGCGTGTGAGAACGAGACAGGACAGGACAGCTAGCG 12840
Db 12781 ACCGCGAACCGGTTTGAAAGAGCGTGTGAGAACGAGACAGGACAGGACAGCTAGCG 12840
QY 12841 GCGCCCGACGCTCAGTTCGCTACGACAGCTCCGCGGACGATCAACAAAGTGTGAG 12900
Db 12841 GCGCCCGACGCTCAGTTCGCTACGACAGCTCCGCGGACGATCAACAAAGTGTGAG 12900
QY 12901 GAGCTCTCCAGGCGGTGTGCGAGAAACGAGTGAAGGACACCTACATGTGTAGCAATG 12960
Db 12901 GAGCTCTCCAGGCGGTGTGCGAGAAACGAGTGAAGGACACCTACATGTGTAGCAATG 12960
QY 12961 AGCAAGATTAACCCCAACGAGCTAATGACGGGATATACGGGCGCGGTGTGCGGCAAG 13020
Db 12961 AGCAAGATTAACCCCAACGAGCTAATGACGGGATATACGGGCGCGGTGTGCGGCAAG 13020
QY 13021 TTCGTGGGCGAGCCATCTCCGTGACGAGCTCGTGGGCGGTGAGACAGGCGTCCGTACG 13080
Db 13021 TTCGTGGGCGAGCCATCTCCGTGACGAGCTCGTGGGCGGTGAGACAGGCGTCCGTACG 13080

QY 13081 ATCCACAGAGCCCTCCGACGTCACCCCGGGGATGCTACTGCGGCCCCCGGGTACG 13140
DB 13081 ATCCACAGAGCCCTCCGACGTCACCCCGGGGATGCTACTGCGGCCCCCGGGTACG 13140
QY 13141 TTCAGGTTCTCAACACACACACGCTGTTCAAGGGCCAGCTGGAGCCAGAAAGAGATC 13200
DB 13141 TTCAGGTTCTCAACACACACACGCTGTTCAAGGGCCAGCTGGAGCCAGAAAGAGATC 13200
QY 13301 ATACTGACGACAAACAGGTGGAGGCGTGCAGAGAGACGTGCGAACACTACTTATAGCG 13260
DB 13301 ATACTGACGACAAACAGGTGGAGGCGTGCAGAGAGACGTGCGAACACTACTTATAGCG 13260
QY 13361 AGCAAGCTAACCTCTACTCAAAAGACTAGCTCTGCGAAAAAATTAACACTCCGAG 13320
DB 13361 AGCAAGCTAACCTCTACTCAAAAGACTAGCTCTGCGAAAAAATTAACACTCCGAG 13320
QY 13321 ATATCCACCTCGGTAGCTTCATCGCCCTGAACCTGTCTTTATAGAAACATGATTTTC 13380
DB 13321 ATATCCACCTCGGTAGCTTCATCGCCCTGAACCTGTCTTTATAGAAACATGATTTTC 13380
QY 13381 AGGGTCAATCGAGCTGTACAGCCGCGGAGAAAAAGCTGTCCGGAGCGTTTGTATATA 13440
DB 13381 AGGGTCAATCGAGCTGTACAGCCGCGGAGAAAAAGCTGTCCGGAGCGTTTGTATATA 13440
QY 13441 GAAACCATGTTCAAGGAATCAACTACTACTACACGACGCGCGGGGACTCCGGAGAGAC 13500
DB 13441 GAAACCATGTTCAAGGAATCAACTACTACTACACGACGCGCGGGGACTCCGGAGAGAC 13500
QY 13501 CTGGACAAACAGATCGACTGAACCCGACCGCCTGGCCCGCGACCTGTCCGAGATAGTC 13560
DB 13501 CTGGACAAACAGATCGACTGAACCCGACCGCCTGGCCCGCGACCTGTCCGAGATAGTC 13560
QY 13561 GCGGACCTGGGCGATGTGCGCCGACGGTGTAACTGACGTGCGCACTAGCTGATTAACCTG 13620
DB 13561 GCGGACCTGGGCGATGTGCGCCGACGGTGTAACTGACGTGCGCACTAGCTGATTAACCTG 13620
QY 13621 TTGCGATCAATCGTGAGCGGGGTTTCACTTAATAAGATGCGTTCCGGGGGCAATGCTC 13680
DB 13621 TTGCGATCAATCGTGAGCGGGGTTTCACTTAATAAGATGCGTTCCGGGGGCAATGCTC 13680
QY 13681 ATGATCTGTGATTTGTGGGGGTCCTGATCGTGTGGCGTAAACCCGGCGACCAAC 13740
DB 13681 ATGATCTGTGATTTGTGGGGGTCCTGATCGTGTGGCGTAAACCCGGCGACCAAC 13740
QY 13741 GCCATGCCCGGACGCCCATCAGATGATCTACCCCGACATAGCAAAATGACACCTCT 13800
DB 13741 GCCATGCCCGGACGCCCATCAGATGATCTACCCCGACATAGCAAAATGACACCTCT 13800
QY 13801 GCGCGTAAAGTCGACAGAGACAGATTAAAAACAATTCTGCGCGGATGACACACTACAG 13860
DB 13801 GCGCGTAAAGTCGACAGAGACAGATTAAAAACAATTCTGCGCGGATGACACACTACAG 13860
QY 13861 CAGGAGAGCGGTAGCGGTTAGAGCAACAGAGAGTCAAGCGCCCTGCTTTCGGCGGC 13920
DB 13861 CAGGAGAGCGGTAGCGGTTAGAGCAACAGAGAGTCAAGCGCCCTGCTTTCGGCGGC 13920
QY 13921 GCGTCAGACGAGCTAAACGTCGTTTAGGGGATTAACCGGTGAAAAAGAGAGCT 13980
DB 13921 GCGTCAGACGAGCTAAACGTCGTTTAGGGGATTAACCGGTGAAAAAGAGAGCT 13980
QY 13981 CAAGAGTATGAATGAGCAATAACACACACACGCTGATCTTTCGGCGCGCGAGAG 14040
DB 13981 CAAGAGTATGAATGAGCAATAACACACACACGCTGATCTTTCGGCGCGCGAGAG 14040
QY 14041 CCGCGGCGCAATGATTCGCGCACCGCGCGGTCCTCCGACACCTCTAGCGCCCGCGG 14100
DB 14041 CCGCGGCGCAATGATTCGCGCACCGCGCGGTCCTCCGACACCTCTAGCGCCCGCGG 14100
QY 14101 CGTCCGGGCTGTATCAATCATGATTTCTTAAACCGGTACGTTGGGCCCTCGCGGACCA 14160
DB 14101 CGTCCGGGCTGTATCAATCATGATTTCTTAAACCGGTACGTTGGGCCCTCGCGGACCA 14160

QY 14161 CGCCCCACTACACAGAGGACCGGATGCTCCGCCCTGCGGGCGGAGCGGTTACG 14220
DB 14161 CGCCCCACTACACAGAGGACCGGATGCTCCGCCCTGCGGGCGGAGCGGTTACG 14220
QY 14221 CCGGCACAGAGCTTTGCAAGGCTCATCCCGCTGCTTCGAAACGCAAGGGGAGCGGG 14280
DB 14221 CCGGCACAGAGCTTTGCAAGGCTCATCCCGCTGCTTCGAAACGCAAGGGGAGCGGG 14280
QY 14281 ATGATCCCGGTACAGATCCGCTTCCCGCAACGACTTTCGAAAGAGGTGCTCGGGAGAC 14340
DB 14281 ATGATCCCGGTACAGATCCGCTTCCCGCAACGACTTTCGAAAGAGGTGCTCGGGAGAC 14340
QY 14341 GTGCTGCTGCGCAACGAAGGCTCATGTGAGCGGCGGCGCAACGCCGTGCGCCG 14400
DB 14341 GTGCTGCTGCGCAACGAAGGCTCATGTGAGCGGCGGCGCAACGCCGTGCGCCG 14400
QY 14401 GACCCCAAGACCAATCCATCAGCTTTCACGCGGTACGAGCTGTTGAAACAGGTACGG 14460
DB 14401 GACCCCAAGACCAATCCATCAGCTTTCACGCGGTACGAGCTGTTGAAACAGGTACGG 14460
QY 14461 GCGGACAGGTGTGCGGAGGTACTAGCCGCTTCCAAACGAGCATTTATCCCAAGGGAAAC 14520
DB 14461 GCGGACAGGTGTGCGGAGGTACTAGCCGCTTCCAAACGAGCATTTATCCCAAGGGAAAC 14520
QY 14521 GTGCTCAAGCTCTGGGGCGCAACCGAGGACGACCAAGCGTGTGAGTACGTTCCTG 14580
DB 14521 GTGCTCAAGCTCTGGGGCGCAACCGAGGACGACCAAGCGTGTGAGTACGTTCCTG 14580
QY 14581 CAACAGTATATTTCTACGCGAAGTTTCACGCGGCAATTAACGTACCCACATCTCCAG 14640
DB 14581 CAACAGTATATTTCTACGCGAAGTTTCACGCGGCAATTAACGTACCCACATCTCCAG 14640
QY 14641 CAGGCTCTCAAGAACACAGCGCGCGCTGCGCGCTGCTGACCAAGAAAGTAAAC 14700
DB 14641 CAGGCTCTCAAGAACACAGCGCGCGCTGCGCGCTGCTGACCAAGAAAGTAAAC 14700
QY 14701 AAAAGAAATTCACAAAGGTAACGAGCTGCGGAGATCCCGTCACAGAAATACACTATCG 14760
DB 14701 AAAAGAAATTCACAAAGGTAACGAGCTGCGGAGATCCCGTCACAGAAATACACTATCG 14760
QY 14761 TCCGTTTCATGCTCTGACCTCAGGACCGCTGCGGCTGCGGCTGCGGAGTGTTC 14820
DB 14761 TCCGTTTCATGCTCTGACCTCAGGACCGCTGCGGCTGCGGCTGCGGAGTGTTC 14820
QY 14821 GAGTCAAAACGAGGAGCGGCTGCGCGGCTGCTGATGATCAAGGTTTACACAGTGGGG 14880
DB 14821 GAGTCAAAACGAGGAGCGGCTGCGCGGCTGCTGATGATCAAGGTTTACACAGTGGGG 14880
QY 14881 TGCTACTGCTGCGCGCGCGCCCGCTGCGGCGGCAAGATGCGAGAGCGCCCTG 14940
DB 14881 TGCTACTGCTGCGCGCGCGCCCGCTGCGGCGGCAAGATGCGAGAGCGCCCTG 14940
QY 14941 GAGTTTGAATGACGCTGGGAGAGCTCAGGTTCAAGCGGACCGCAGGAGTGGCCCGG 15000
DB 14941 GAGTTTGAATGACGCTGGGAGAGCTCAGGTTCAAGCGGACCGCAGGAGTGGCCCGG 15000
QY 15001 TACGCAATCGGCGCTTGAATGAGAGTCACTGGAAGAGGGGGAATTCGTTGGGCAAG 15060
DB 15001 TACGCAATCGGCGCTTGAATGAGAGTCACTGGAAGAGGGGGAATTCGTTGGGCAAG 15060
QY 15061 CCGCAGCGCGAGCGGCTGATCAAGATCTCAGCTCTTCTACAGAGACGAGAGCGCG 15120
DB 15061 CCGCAGCGCGAGCGGCTGATCAAGATCTCAGCTCTTCTACAGAGACGAGAGCGCG 15120
QY 15121 CCAATCCGCCAAACATACCTGTTAGAGTGTGGGACGTGCAACCCATCCCGAGACGAG 15180
DB 15121 CCAATCCGCCAAACATACCTGTTAGAGTGTGGGACGTGCAACCCATCCCGAGACGAG 15180
QY 15181 GTTTGGAGTTTCGTTGGGAAATGACATGTTGGTGTGCTTCCGCAATGATCCGGAGC 15240
DB 15181 GTTTGGAGTTTCGTTGGGAAATGACATGTTGGTGTGCTTCCGCAATGATCCGGAGC 15240
QY 15241 TTCAGAGTGAATTTTAAACCGGCTATTAACATCTCAAACTTGATCTCCGTAATTC 15300

Db	16321	CGAACGGCTCGCGGTCCGGAGGTACACCGCCCGTCACGGCCGCGGTTTCGGCTGCTTAC	16380
Qy	16381	GGTGACACAGCACTCCCTTTATTCGCGTGGACGGTATTTCGCCGAGAGCCCTTTCGGCT	16440
Db	16381	GGTGACACAGCACTCCCTTTATTCGCGTGGACGGTATTTCGCCGAGAGCCCTTTCGGCT	16440
Qy	16441	TTCTGTACGATCTGGCCGCCAGGATCATCGGAGCTGTTCGCCCACTTAAGCTA	16500
Db	16441	TTCTGTACGATCTGGCCGCCAGGATCATCGGAGCTGTTCGCCCACTTAAGCTA	16500
Qy	16501	GAGGGGAAAGACGTTCAAGTGTCTCTGCTGTGCGAAAAAGGCTACATCGGGGGTC	16560
Db	16501	GAGGGGAAAGACGTTCAAGTGTCTCTGCTGTGCGAAAAAGGCTACATCGGGGGTC	16560
Qy	16561	CTATTGACGACAAATATGTCATGAAGGGGTGCAGCTCATTCGCAAAAGCCTCTCAAG	16620
Db	16561	CTATTGACGACAAATATGTCATGAAGGGGTGCAGCTCATTCGCAAAAGCCTCTCAAG	16620
Qy	16621	TTTGTCCAGAGCGATGCGCGCCATCTGAGCTGTGCTCCAGATCCGAGGTCAAG	16680
Db	16621	TTTGTCCAGAGCGATGCGCGCCATCTGAGCTGTGCTCCAGATCCGAGGTCAAG	16680
Qy	16681	GCTCGGGGGCGGCTGTGTGTGCAACGGGCGCCGACGGGTATACGAGAGAGGGGCTCGCG	16740
Db	16681	GCTCGGGGGCGGCTGTGTGTGCAACGGGCGCCGACGGGTATACGAGAGAGGGGCTCGCG	16740
Qy	16741	GCTGGCTTTATTAATAATCTGTAGAGGTCTCTAACGCGAGCTATCTGAGACTCCGAAACAGC	16800
Db	16741	GCTGGCTTTATTAATAATCTGTAGAGGTCTCTAACGCGAGCTATCTGAGACTCCGAAACAGC	16800
Qy	16801	GTCGTGCCCATTCGAGCAGTTAAGCTGTCTCCACGAGCTCAGCCGCCCTGTGCGATTAC	16860
Db	16801	GTCGTGCCCATTCGAGCAGTTAAGCTGTCTCCACGAGCTCAGCCGCCCTGTGCGATTAC	16860
Qy	16861	AAGACCCACCAACCTGCCCCACCTGGGGGTCTACCAAAAGCTGGCGAGCGTGCAGAGAG	16920
Db	16861	AAGACCCACCAACCTGCCCCACCTGGGGGTCTACCAAAAGCTGGCGAGCGTGCAGAGAG	16920
Qy	16921	CTGCCCCAGGTGACGATAGAAATCCCTAGCTGTTCGTGGACGCGCCGGGTCCCTAAG	16980
Db	16921	CTGCCCCAGGTGACGATAGAAATCCCTAGCTGTTCGTGGACGCGCCGGGTCCCTAAG	16980
Qy	16981	TCGGAACCTGGCCGAACACCCGGATTACGTGACAGACACAGATTCCCGTCCGGGTGCAC	17040
Db	16981	TCGGAACCTGGCCGAACACCCGGATTACGTGACAGACACAGATTCCCGTCCGGGTGCAC	17040
Qy	17041	CTATATTTCGACAAACGTGTGACGCGGGGCCAACAATCTCCAGTGTCTGTTCCGGCAAC	17100
Db	17041	CTATATTTCGACAAACGTGTGACGCGGGGCCAACAATCTCCAGTGTCTGTTCCGGCAAC	17100
Qy	17101	AACCGGACACACAGGTGGCCATCTCTACAAATTTTCTCAAGTCCCGGTAAAGCTGTC	17160
Db	17101	AACCGGACACACAGGTGGCCATCTCTACAAATTTTCTCAAGTCCCGGTAAAGCTGTC	17160
Qy	17161	TCGTGAACGCCAATTGAGAGGCCCAATPAAGACGCCGCCGACGGAGTCCGACAGGA	17220
Db	17161	TCGTGAACGCCAATTGAGAGGCCCAATPAAGACGCCGCCGACGGAGTCCGACAGGA	17220
Qy	17221	GAGCTCGAGGGGGAGAGAGGACCAACGAGACCGGCACCATGTGTGAAGAACTGTC	17280
Db	17221	GAGCTCGAGGGGGAGAGAGGACCAACGAGACCGGCACCATGTGTGAAGAACTGTC	17280
Qy	17281	GGTGGTCTCTGGGGGACGTGGGAGGTGACTTTTACCGGGGTAGATTACGTTGCTCAACCT	17340
Db	17281	GGTGGTCTCTGGGGGACGTGGGAGGTGACTTTTACCGGGGTAGATTACGTTGCTCAACCT	17340
Qy	17341	CACCCGCCTCGAAACGTTCAAGGGCCACAGGGGGCTACGCGAGGTCGCACTCCCTTCTC	17400
Db	17341	CACCCGCCTCGAAACGTTCAAGGGCCACAGGGGGCTACGCGAGGTCGCACTCCCTTCTC	17400
Qy	17401	GCTCGACCAAGTACTCCACCAACATTTTCGGCTTCGAGCTGTGAGCGGCTCTAAGAACT	17460
Db	17401	GCTCGACCAAGTACTCCACCAACATTTTCGGCTTCGAGCTGTGAGCGGCTCTAAGAACT	17460

|||||
Db 19621 TTGGGTGGCCCGGAAATGCGGACGCTCTGGCCACCGATCGGCGCCGAGCTG 19680
Qy 19681 CCGGGGGGGGTGACAGTGCACAGCCAAAACCTGTGATGTTGAGACCATGTACCTGTTT 19740
Db 19681 CCGGGGGGGGTGACAGTGCACAGCCAAAACCTGTGATGTTGAGACCATGTACCTGTTT 19740
Qy 19741 TCCACGTAAATTAATAAACCCTGTTGCTCGTATCGCTCACAAACGCCAAACCGTCTC 19800
Db 19741 TCCACGTAAATTAATAAACCCTGTTGCTCGTATCGCTCACAAACGCCAAACCGTCTC 19800
Qy 19801 TCATTTCCGGGGTGGCGCGCCCTGCGAACAACAGGTGGCTCAACACCCCTCCCGC 19860
Db 19801 TCATTTCCGGGGTGGCGCGCCCTGCGAACAACAGGTGGCTCAACACCCCTCCCGC 19860
Qy 19861 ACCCTGCCACACAAAACAGTTAACGCCCTCCGTTAGATGCAGTTATTTATTTTAA 19920
Db 19861 ACCCTGCCACACAAAACAGTTAACGCCCTCCGTTAGATGCAGTTATTTATTTTAA 19920
Qy 19921 TTACATCATAGTATTTGGCGGCGCCGCTCCGCAAAAACATCTGTAGATATTCAGTAT 19980
Db 19921 TTACATCATAGTATTTGGCGGCGCCGCTCCGCAAAAACATCTGTAGATATTCAGTAT 19980
Qy 19981 GCGAAACGGGCTGAGAAACAGTCGCGGGGGCTGTGCTCCCAAGCGACGCGGTTT 20040
Db 19981 GCGAAACGGGCTGAGAAACAGTCGCGGGGGCTGTGCTCCCAAGCGACGCGGTTT 20040
Qy 20041 TTCAATTAGATCCCGCCACACTATCTTGTATTATTTACGGGNAAGCTCCCTCAATTAGAGATC 20100
Db 20041 TTCAATTAGATCCCGCCACACTATCTTGTATTATTTACGGGNAAGCTCCCTCAATTAGAGATC 20100
Qy 20101 GAGGGGGGACAGACACAGGTGACCGCGGAGCCAAATGCGCGGCTCCGCGTCCCGG 20160
Db 20101 GAGGGGGGACAGACACAGGTGACCGCGGAGCCAAATGCGCGGCTCCGCGTCCCGG 20160
Qy 20161 CCGGTGTCCAGACAGCATCTGATGTCGCGTCAAGTACTGTGTAGCCCGGAGCCGCG 20220
Db 20161 CCGGTGTCCAGACAGCATCTGATGTCGCGTCAAGTACTGTGTAGCCCGGAGCCGCG 20220
Qy 20221 AACCATGGCGTTCATACACTCGGCGCCGGAACCTGCGGCGCTGGCACTCAACGTTAGA 20280
Db 20221 AACCATGGCGTTCATACACTCGGCGCCGGAACCTGCGGCGCTGGCACTCAACGTTAGA 20280
Qy 20281 CATCATATATGGAATGTAACAACAGCATGATGCGCGGGTACTGACGACCCGACAGAG 20340
Db 20281 CATCATATATGGAATGTAACAACAGCATGATGCGCGGGTACTGACGACCCGACAGAG 20340
Qy 20341 AGTGAAGTGTGGACAGGTAAACGAACGAGCGCTGTATGTTTAAACCCCACTTCAGACAG 20400
Db 20341 AGTGAAGTGTGGACAGGTAAACGAACGAGCGCTGTATGTTTAAACCCCACTTCAGACAG 20400
Qy 20401 GCGCCCTCTGCTCTGTCAAGAGAGCGGCTGTGCGGCCCACTGGGGGAGAACTGTAAT 20460
Db 20401 GCGCCCTCTGCTCTGTCAAGAGAGCGGCTGTGCGGCCCACTGGGGGAGAACTGTAAT 20460
Qy 20461 TCCAGGCGAGTTCGGGGGAGGCGCCAGCTAGGCGCTGCGGCCCAACAGACAGATGTAAT 20520
Db 20461 TCCAGGCGAGTTCGGGGGAGGCGCCAGCTAGGCGCTGCGGCCCAACAGACAGATGTAAT 20520
Qy 20521 CAAAGAGAACAGACAGGGAACATGACCGGTTAAATTAATCTGCTTCAATTCGCGGCGGC 20580
Db 20521 CAAAGAGAACAGACAGGGAACATGACCGGTTAAATTAATCTGCTTCAATTCGCGGCGGC 20580
Qy 20581 GCGCGGTCAAGCGCAGGTCAATTAAACACACCGCGCCCAACCCCAACCGCGGCGCG 20640
Db 20581 GCGCGGTCAAGCGCAGGTCAATTAAACACACCGCGCCCAACCCCAACCGCGGCGCG 20640
Qy 20641 CCGCCCTGGAACCGGCTCTTCCATTCGGAAGAACCGGCTGACAAAAGGCGCTGTTT 20700
Db 20641 CCGCCCTGGAACCGGCTCTTCCATTCGGAAGAACCGGCTGACAAAAGGCGCTGTTT 20700
Qy 20701 GAACCATTTTGTGCATCGGGTTGTTTTCAGATACGGAAGCGCTGTCCAAAACA 20760
Db 20701 GAACCATTTTGTGCATCGGGTTGTTTTCAGATACGGAAGCGCTGTCCAAAACA 20760

Db 20701 GAACCATTTTGTGCATCGGGTTGTTTTCAGATACGGAAGCGCTGTCCAAAACA 20760
Qy 20761 CCCAAGGGGGTGTGCTCAAAACGCCCATCTCATCTATGTGAGGATGGGGTCTGTAC 20820
Db 20761 CCCAAGGGGGTGTGCTCAAAACGCCCATCTCATCTATGTGAGGATGGGGTCTGTAC 20820
Qy 20821 CCTGAGACTCAGATCCGCGCGGTAAAGTCTCTCAGACGCGCCACTTTCCTCAAAATCT 20880
Db 20821 CCTGAGACTCAGATCCGCGCGGTAAAGTCTCTCAGACGCGCCACTTTCCTCAAAATCT 20880
Qy 20881 TCAGCGCGGAAAGGACCGGGGCTCTCCGACGCTGGAAGGACGACGAGGATCAAGTGGT 20940
Db 20881 TCAGCGCGGAAAGGACCGGGGCTCTCCGACGCTGGAAGGACGACGAGGATCAAGTGGT 20940
Qy 20941 TGTGTTAAACGTTGGGCGGTACCCCAAGGTGTGCACAAAGTCTCCGGGGTCAAGCCGCTGA 21000
Db 20941 TGTGTTAAACGTTGGGCGGTACCCCAAGGTGTGCACAAAGTCTCCGGGGTCAAGCCGCTGA 21000
Qy 21001 CGTGAGCGATCAGATACGTACAGAGGGGCTAGCTGGCGATGTTAAACGGGACCCGAGGC 21060
Db 21001 CGTGAGCGATCAGATACGTACAGAGGGGCTAGCTGGCGATGTTAAACGGGACCCGAGGC 21060
Qy 21061 CCATGTGCGGGACCTCTGCTACAGCTGGCAGAGACGCTCCCGGAGCCAGCTAAACT 21120
Db 21061 CCATGTGCGGGACCTCTGCTACAGCTGGCAGAGACGCTCCCGGAGCCAGCTAAACT 21120
Qy 21121 GACACAAAACGTGACAAAGAGGAGAGCCATCCGCGGAGGTCCGCGGGGTTCCAGCGC 21180
Db 21121 GACACAAAACGTGACAAAGAGGAGAGCCATCCGCGGAGGTCCGCGGGGTTCCAGCGC 21180
Qy 21181 ACATTAACGATGGCGCGATGCTGGGGCGCGCTGTATTATGATTCACACAGTAAACGAGT 21240
Db 21181 ACATTAACGATGGCGCGATGCTGGGGCGCGCTGTATTATGATTCACACAGTAAACGAGT 21240
Qy 21241 GGTCCACCCCTGACCCCTGCTGATGTTGGCTGCGGCCCTGTACTGACGCGCCCAAAATGTC 21300
Db 21241 GGTCCACCCCTGACCCCTGCTGATGTTGGCTGCGGCCCTGTACTGACGCGCCCAAAATGTC 21300
Qy 21301 TCCACTGGAACCCGTAACACCGGCGCCAGATGCGCCCTGCGGCGGTCCCGAAGCCCTGCG 21360
Db 21301 TCCACTGGAACCCGTAACACCGGCGCCAGATGCGCCCTGCGGCGGTCCCGAAGCCCTGCG 21360
Qy 21361 CCGCCAAAAGGCGGGGACCCGCTGCGGCTCCCAATTTTAAACGCGGCGCGACAGT 21420
Db 21361 CCGCCAAAAGGCGGGGACCCGCTGCGGCTCCCAATTTTAAACGCGGCGCGACAGT 21420
Qy 21421 CCGTGAAGTGGGTGAGCGCCCTGATTAACACAGCAACGACCTCCACAGACGCCCTCCAAA 21480
Db 21421 CCGTGAAGTGGGTGAGCGCCCTGATTAACACAGCAACGACCTCCACAGACGCCCTCCAAA 21480
Qy 21481 ACACCTTTTGTGTTAAACAGAGAACTCTCCCTGAGTTAATGCGGCTCAAGC 21540
Db 21481 ACACCTTTTGTGTTAAACAGAGAACTCTCCCTGAGTTAATGCGGCTCAAGC 21540
Qy 21541 CGAACAGGAGCTGTGGCCCAAGCGCGCTGCTCCCTGACAGCGCGGTAAATTA 21600
Db 21541 CGAACAGGAGCTGTGGCCCAAGCGCGCTGCTCCCTGACAGCGCGGTAAATTA 21600
Qy 21601 TTAATTCAGAGTGGCGCAAGTACTGAGCTGCGCTGTGCGCGGACGCGACGCGA 21660
Db 21601 TTAATTCAGAGTGGCGCAAGTACTGAGCTGCGCTGTGCGCGGACGCGACGCGA 21660
Qy 21661 CCGCGCGGCGACCTTCGCGGTGCGGAAAAAACCCCGAGTGTGCGCGCGGATTCAGCGA 21720
Db 21661 CCGCGCGGCGACCTTCGCGGTGCGGAAAAAACCCCGAGTGTGCGCGCGGATTCAGCGA 21720
Qy 21721 CGCAAAACGGGTAAATTTTAAACGTAAGTACGAGTACGAGTACGAGTACGAGTACGAGT 21780
Db 21721 CGCAAAACGGGTAAATTTTAAACGTAAGTACGAGTACGAGTACGAGTACGAGTACGAGT 21780
Qy 21781 TTACAACGAGGTGCTTTACAACATTAACCGGTAACCGGCTGAAAGCGAACTTATTTTAA 21840
Db 21781 TTACAACGAGGTGCTTTACAACATTAACCGGTAACCGGCTGAAAGCGAACTTATTTTAA 21840

QY 21841 AGGCACTTGGGCGGGCGGACACAGGCGGCGCGCTGTACGATATTAACCA 21900
|||||
Db 21841 AGGCACTTGGGCGGGCGGACACAGGCGGCGCGCTGTACGATATTAACCA 21900
QY 21901 CGTGTCTCCCAAGCGTCTCCCGAGCGTGAAGCTCTCCCAAGCGCAACAC 21960
|||||
Db 21901 CGTGTCTCCCAAGCGTCTCCCGAGCGTGAAGCTCTCCCAAGCGCAACAC 21960
QY 21961 AGATATATAAATAAATACATGTATTTTATTAATACCTTAAGCGGATTTAGTCTCT 22020
|||||
Db 21961 AGATATATAAATAAATACATGTATTTTATTAATACCTTAAGCGGATTTAGTCTCT 22020
QY 22021 AACAGGGGCAATAGAACAGACGTGAGGCGGATTTGCGCGCTCAAAAGCAACGCA 22080
|||||
Db 22021 AACAGGGGCAATAGAACAGACGTGAGGCGGATTTGCGCGCTCAAAAGCAACGCA 22080
QY 22081 CACCGGCGCTGTAACAGCGTAAACAAACACTATTAGCATTTGCTAAACGTAATCCA 22140
|||||
Db 22081 CACCGGCGCTGTAACAGCGTAAACAAACACTATTAGCATTTGCTAAACGTAATCCA 22140
QY 22141 ACCCTGCGTCCGAGCATTCGCGAGCTGCTACGTGAGGCGTCTTAAGTCG 22200
|||||
Db 22141 ACCCTGCGTCCGAGCATTCGCGAGCTGCTACGTGAGGCGTCTTAAGTCG 22200
QY 22201 CATTTGAGCCCTTGGCAGCGCGGCTGCTTAATGGTGTCTTAATCCCGCTGCCA 22260
|||||
Db 22201 CATTTGAGCCCTTGGCAGCGCGGCTGCTTAATGGTGTCTTAATCCCGCTGCCA 22260
QY 22261 AGGCGCTCTTGGAAATCGTAATCAAGCGTGGCGGGTCTCTGCGCTTTTGGGAGCG 22320
|||||
Db 22261 AGGCGCTCTTGGAAATCGTAATCAAGCGTGGCGGGTCTCTGCGCTTTTGGGAGCG 22320
QY 22321 TTGTCACCGCGCTGAAGAGTTCTTCACTGCTGCTCCCGGGATTTGGCAACAGCTTT 22380
|||||
Db 22321 TTGTCACCGCGCTGAAGAGTTCTTCACTGCTGCTCCCGGGATTTGGCAACAGCTTT 22380
QY 22381 TTACGCGGCGAGTGTATTAATCAAGGCGTCCACGAGCACTGGGAGAGTGTGGGAG 22440
|||||
Db 22381 TTACGCGGCGAGTGTATTAATCAAGGCGTCCACGAGCACTGGGAGAGTGTGGGAG 22440
QY 22441 TAAGAGACCACTAAACCGGGTGGCGGAGATGATTACATACCCCAACAGCAGATTCG 22500
|||||
Db 22441 TAAGAGACCACTAAACCGGGTGGCGGAGATGATTACATACCCCAACAGCAGATTCG 22500
QY 22501 GCGGGGGGCGCTATGAGAGCCATPAGGAAGGATATCAACTACACAGCGAAGCC 22560
|||||
Db 22501 GCGGGGGGCGCTATGAGAGCCATPAGGAAGGATATCAACTACACAGCGAAGCC 22560
QY 22561 GCAAAAAAAGCGCACAGCAAGAAAGGCCCTCATGTGACAAACAAACAAAGAGCGG 22620
|||||
Db 22561 GCAAAAAAAGCGCACAGCAAGAAAGGCCCTCATGTGACAAACAAACAAAGAGCGG 22620
QY 22621 GTCGCTCGTGTGCGCACACAGCGCGCTGCGCGTGGCCAGGTTAGCGCGCTC 22680
|||||
Db 22621 GTCGCTCGTGTGCGCACACAGCGCGCTGCGCGTGGCCAGGTTAGCGCGCTC 22680
QY 22681 CATTAATACCGCGGCGCGGCGCTGCGAGCAAGCGGCGGTTAGCAGCTGAC 22740
|||||
Db 22681 CATTAATACCGCGGCGCGGCGCTGCGAGCAAGCGGCGGTTAGCAGCTGAC 22740
QY 22741 GCAGGTGCTCCCGCTCAGATGTGGCATTTGGAGTCCCAAAAGCGGCGTCTAACTACG 22800
|||||
Db 22741 GCAGGTGCTCCCGCTCAGATGTGGCATTTGGAGTCCCAAAAGCGGCGTCTAACTACG 22800
QY 22801 GTCGCGCGGCGGTTCAAGAACAGGAGATCCCAAAACAGGTAAGGCTTTTGTCCAA 22860
|||||
Db 22801 GTCGCGCGGCGGTTCAAGAACAGGAGATCCCAAAACAGGTAAGGCTTTTGTCCAA 22860
QY 22861 CAGAAAGCCACAGCAAGCAAGGAAATGTCAAAACAGCAAGGATCCGTCGCGGCA 22920
|||||
Db 22861 CAGAAAGCCACAGCAAGCAAGGAAATGTCAAAACAGCAAGGATCCGTCGCGGCA 22920

QY 22921 TAAACGAAATTTTCCCTCACCTTAACACAGCGCGCGGCTAACTGTATAAACAGCAAT 22980
|||||
Db 22921 TAAACGAAATTTTCCCTCACCTTAACACAGCGCGCGGCTAACTGTATAAACAGCAAT 22980
QY 22981 ACTTCTAGGCTGTGTTTAAATAACACAGAGGTTGTATTTTCGGGGGCGCTTTGG 23040
|||||
Db 22981 ACTTCTAGGCTGTGTTTAAATAACACAGAGGTTGTATTTTCGGGGGCGCTTTGG 23040
QY 23041 GCCCGGCGGCTGAGGGGCGGCTGTCGTTGTGTTGCAATACCAACCGCGCTGCG 23100
|||||
Db 23041 GCCCGGCGGCTGAGGGGCGGCTGTCGTTGTGTTGCAATACCAACCGCGCTGCG 23100
QY 23101 CGAAAAACAGGCGCAACCGCGCTGCTAGTTTAAAACTTAACACCGGCAAGGGA 23160
|||||
Db 23101 CGAAAAACAGGCGCAACCGCGCTGCTAGTTTAAAACTTAACACCGGCAAGGGA 23160
QY 23161 GAGGAGAAAGGGGTGCGGCTTAATGGCTGTTAGACGCAACCGCAGGCGGGAAGAAAG 23220
|||||
Db 23161 GAGGAGAAAGGGGTGCGGCTTAATGGCTGTTAGACGCAACCGCAGGCGGGAAGAAAG 23220
QY 23221 GGGCAAGCGCGGTTAACACAAACAGCAAGCGCGCAACCAATTAACACAAGCA 23280
|||||
Db 23221 GGGCAAGCGCGGTTAACACAAACAGCAAGCGCGCAACCAATTAACACAAGCA 23280
QY 23281 TATTCGTTGTGTTTCGCGGCGCGGCTGCTAACCGCGCTTGGCGTTGCA 23340
|||||
Db 23281 TATTCGTTGTGTTTCGCGGCGCGGCTGCTAACCGCGCTTGGCGTTGCA 23340
QY 23341 AGCAGCGCGCGCGCTGCACCGCGCTCCCGAGGTCACCGAAGGCTCAGGAACATAGT 23400
|||||
Db 23341 AGCAGCGCGCGCGCTGCACCGCGCTCCCGAGGTCACCGAAGGCTCAGGAACATAGT 23400
QY 23401 TTACAGGTCGCAAGTCGCGCGGCTGTCGCAACATCTTTCGCTGCTCCGAAACCGGGA 23460
|||||
Db 23401 TTACAGGTCGCAAGTCGCGCGGCTGTCGCAACATCTTTCGCTGCTCCGAAACCGGGA 23460
QY 23461 AAATCCCGCGCGCGGCTGCTGGAAGGCGCGGAAGATATCCCAACGCAACTA 23520
|||||
Db 23461 AAATCCCGCGCGCGGCTGCTGGAAGGCGCGGAAGATATCCCAACGCAACTA 23520
QY 23521 AAGCATCATGTTTGGGGTTTCGCTGACGCGCGCGCAAGAGGCGCGGTGGCGCTG 23580
|||||
Db 23521 AAGCATCATGTTTGGGGTTTCGCTGACGCGCGCGCAAGAGGCGCGGTGGCGCTG 23580
QY 23581 CGAAGATAGTGGCGCGCAGAGCAAGGCTTTCGCTAGACGCGCTGAGCGCTGCACCT 23640
|||||
Db 23581 CGAAGATAGTGGCGCGCAGAGCAAGGCTTTCGCTAGACGCGCTGAGCGCTGCACCT 23640
QY 23641 GGCAGCAGCGCAAAACACAGGCGCGCGAGCGCGGCGGAGGTTGGCGCGCTTTCCCG 23700
|||||
Db 23641 GGCAGCAGCGCAAAACACAGGCGCGCGAGCGCGGCGGAGGTTGGCGCGCTTTCCCG 23700
QY 23701 CACGCGCGATTTGGCAAAATGCGGACCGGAGCGCGGTTGGAGCGCGCGACTCA 23760
|||||
Db 23701 CACGCGCGATTTGGCAAAATGCGGACCGGAGCGCGGTTGGAGCGCGCGACTCA 23760
QY 23761 TCACAGGAGAGAGCGCAGTGTGCTCACTTTCGCTCAATCACAGAGCGCGCGCG 23820
|||||
Db 23761 TCACAGGAGAGAGCGCAGTGTGCTCACTTTCGCTCAATCACAGAGCGCGCGCG 23820
QY 23821 TTGGCGGATATATGAACCGGCGCGCATTTGAGCGGCGGCAACCAATGGCGCT 23880
|||||
Db 23821 TTGGCGGATATATGAACCGGCGCGCATTTGAGCGGCGGCAACCAATGGCGCT 23880
QY 23881 TTGGGTTTGTATACAGTTCCCTATATATATATATATATCTTCCCTTAAAGGAATC 23940
|||||
Db 23881 TTGGGTTTGTATACAGTTCCCTATATATATATATATATCTTCCCTTAAAGGAATC 23940
QY 23941 CCATGTTCTTAATCAATCACTGGGTTATATATATATATATATATATATATATAT 24000
|||||
Db 23941 CCATGTTCTTAATCAATCACTGGGTTATATATATATATATATATATATATATAT 24000
QY 24001 TACTGTATTTATTTAATTAATTTATTTATTTATTTATTTAATTAATTTCTTGGCT 24060
|||||

|||||
Db 24001 TACGATTTATTTAAATTTATTTATTTATTTATTTAAATTAATTCCTTCGT 24060
OY 24061 TATATGTAATACATCTAGCTGGGAATCTACTCCAGTTTAAATAAATAATATTAAT 24120
Db 24061 TATATGTAATACATCTAGCTGGGAATCTACTCCAGTTTAAATAAATAATATTAAT 24120
OY 24121 CTATATGATGGGGGCTCTAATAATGTACAAAACAACAATATTTTAAATTTATTCAC 24180
Db 24121 CTATATGATGGGGGCTCTAATAATGTACAAAACAACAATATTTTAAATTTATTCAC 24180
OY 24181 TAAAAATGTCCTTTTACTGTGACGATGTTAGGAATGGGAGTGGTTTGAAC 24240
Db 24181 TAAAAATGTCCTTTTACTGTGACGATGTTAGGAATGGGAGTGGTTTGAAC 24240
OY 24241 TATGTTTCAAAACAACACCTTTTGGGCGCTGTAACATATATACGGAAGCTCGGC 24300
Db 24241 TATGTTTCAAAACAACACCTTTTGGGCGCTGTAACATATATACGGAAGCTCGGC 24300
OY 24301 GTTAATTTGCACTGGCCGCTAACACATCCCTTGGCAGTTGAGTTTATGCTGCTTA 24360
Db 24301 GTTAATTTGCACTGGCCGCTAACACATCCCTTGGCAGTTGAGTTTATGCTGCTTA 24360
OY 24361 TGGCTTACCTCGCATTCGGGGACAAGCTGATTTAGTAGACACGATTTGGGGTTTAA 24420
Db 24361 TGGCTTACCTCGCATTCGGGGACAAGCTGATTTAGTAGACACGATTTGGGGTTTAA 24420
OY 24421 CCGGTTGAATTTATGTTGTCACAGTAAATAAAGCCACGAGGCTTGGGTTTAAACGT 24480
Db 24421 CCGGTTGAATTTATGTTGTCACAGTAAATAAAGCCACGAGGCTTGGGTTTAAACGT 24480
OY 24481 TTTAAGGCTTGTGCTTTTATTAACATGCAATTTATTTATTTAGGAGCTATGTAATTC 24540
Db 24481 TTTAAGGCTTGTGCTTTTATTAACATGCAATTTATTTATTTAGGAGCTATGTAATTC 24540
OY 24541 CGCATGCTTGGGTTTATGTTGTTACAAAACAAGATTTGTAAGCCGAAATTTGTACTGG 24600
Db 24541 CGCATGCTTGGGTTTATGTTGTTACAAAACAAGATTTGTAAGCCGAAATTTGTACTGG 24600
OY 24601 TACCCAAAACGGGACCCGCTTAACACAGCCCGCGCTTGTCTTCTAGCCGC 24660
Db 24601 TACCCAAAACGGGACCCGCTTAACACAGCCCGCGCTTGTCTTCTAGCCGC 24660
OY 24661 TCGCAATACATGCAATTTTAAATTTAAATGGGGCAATGCGCTAGCGCAATTTAAGC 24720
Db 24661 TCGCAATACATGCAATTTTAAATTTAAATGGGGCAATGCGCTAGCGCAATTTAAGC 24720
OY 24721 CGTCAAAATTTAAATGACATACTAACCGGCTTTTATGTAACCTATGGCGAATTTT 24780
Db 24721 CGTCAAAATTTAAATGACATACTAACCGGCTTTTATGTAACCTATGGCGAATTTT 24780
OY 24781 AAAATTTAAAGCCGTGGGTTTAAACACAGAGCTGCGAGCTTGTAAATGTTGCATATACA 24840
Db 24781 AAAATTTAAAGCCGTGGGTTTAAACACAGAGCTGCGAGCTTGTAAATGTTGCATATACA 24840
OY 24841 GTGCGCTTGTGATTTATGTTAGTAAAGTATTTAACTTGAATTTTATATGTTACAC 24900
Db 24841 GTGCGCTTGTGATTTATGTTAGTAAAGTATTTAACTTGAATTTTATATGTTACAC 24900
OY 24901 GTGATTTTAAATGAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAT 24960
Db 24901 GTGATTTTAAATGAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAT 24960
OY 24961 TTAATGTAACATTTGTAATTTTAACTGCTTATGTTATGTTTGTGTTAATTTATGTAAT 25020
Db 24961 TTAATGTAACATTTGTAATTTTAACTGCTTATGTTATGTTTGTGTTAATTTATGTAAT 25020
OY 25021 TTTGCTTTTATGATTTGTTGGGCTGTAATTCAGACAGGTAAGAGCTTACTCTCTATGT 25080
Db 25021 TTTGCTTTTATGATTTGTTGGGCTGTAATTCAGACAGGTAAGAGCTTACTCTCTATGT 25080
OY 25081 TTGCTTTGCGGCTTCTTAAATGTTTGGCTTGGCCGCTTAAAGTTTGGCTTG 25140
Db 25081 TTGCTTTGCGGCTTCTTAAATGTTTGGCTTGGCCGCTTAAAGTTTGGCTTG 25140

|||||
Db 25081 TTGCTTTGCGGCTTCTTAAATGTTTGGCTTGGCCGCTTAAAGTTTGGCTTG 25140
OY 25141 CCGGCTTATGCTTAATTTGCTTGGCGCTAGCTCTAATGTTTGGCTTGGCGCTAG 25200
Db 25141 CCGGCTTATGCTTAATTTGCTTGGCGCTAGCTCTAATGTTTGGCTTGGCGCTAG 25200
OY 25201 CTGCTAATGTTTGGCTTGGCGCTAGCTCTAATGTTTGGCTTGGCGCTAGCTCTAAT 25260
Db 25201 CTGCTAATGTTTGGCTTGGCGCTAGCTCTAATGTTTGGCTTGGCGCTAGCTCTAAT 25260
OY 25261 GTTTGCTTGGCGCTAGCTCTAATGTTTGGCTTGGCGCTAGCTCTAATGTTTGGCT 25320
Db 25261 GTTTGCTTGGCGCTAGCTCTAATGTTTGGCTTGGCGCTAGCTCTAATGTTTGGCT 25320
OY 25321 TGGCGCTAGCTCTAATGTTTGGCTTGGCGCTAGCTCTAATGTTTAAACAATTAAT 25380
Db 25321 TGGCGCTAGCTCTAATGTTTGGCTTGGCGCTAGCTCTAATGTTTAAACAATTAAT 25380
OY 25381 GTTTAAGCACATAAATTTAAAGAGCTTTGTTGTTTATGACACCTTGTATCA 25440
Db 25381 GTTTAAGCACATAAATTTAAAGAGCTTTGTTGTTTATGACACCTTGTATCA 25440
OY 25441 AACCTGCTGATTTTATCCCAACAATAAATAAATAAATAAATAAATAAATAAATAA 25500
Db 25441 AACCTGCTGATTTTATCCCAACAATAAATAAATAAATAAATAAATAAATAAATAA 25500
OY 25501 TTTGCTTGTGTAATTTGGGTTTCCCGAGAGGTCCTCCGCTTCCCGAGAGGTCCTCG 25560
Db 25501 TTTGCTTGTGTAATTTGGGTTTCCCGAGAGGTCCTCCGCTTCCCGAGAGGTCCTCG 25560
OY 25561 GCTTCCCGTTTCCCGAGAGGTCCTCCGCTTCCCGAGAGGTCCTCCGCTTCCCGCTT 25620
Db 25561 GCTTCCCGTTTCCCGAGAGGTCCTCCGCTTCCCGAGAGGTCCTCCGCTTCCCGCTT 25620
OY 25621 CCGGAGAGGTCCTCCGCTTCCCGAGAGGTCCTCCGCTTCCCGAGAGGTCCTCCGAGGT 25680
Db 25621 CCGGAGAGGTCCTCCGCTTCCCGAGAGGTCCTCCGCTTCCCGAGAGGTCCTCCGAGGT 25680
OY 25681 CCGGAGGTCCTTCCCGAGAGGTCCTCCGCTTCCCGAGAGGTCCTCCGAGGTCCTCC 25740
Db 25681 CCGGAGGTCCTTCCCGAGAGGTCCTCCGCTTCCCGAGAGGTCCTCCGAGGTCCTCC 25740
OY 25741 CCGTTCCTCCGAGAGGTCCTCCGCTTCCCGAGAGGTCCTCCGAGGTCCTCCGCTTCC 25800
Db 25741 CCGTTCCTCCGAGAGGTCCTCCGCTTCCCGAGAGGTCCTCCGAGGTCCTCCGCTTCC 25800
OY 25801 AGGGTCCCGGCTTCCCGAGAGGTCCTCCGAGGTCCTCCGAGGTCCTCCGAGGTCCTCG 25860
Db 25801 AGGGTCCCGGCTTCCCGAGAGGTCCTCCGAGGTCCTCCGAGGTCCTCCGAGGTCCTCG 25860
OY 25861 GCTTCCCGTTTCCCGAGAGGTCCTCCGCTTCCCGAGAGGTCCTCCGAGGTCCTCCGCTT 25920
Db 25861 GCTTCCCGTTTCCCGAGAGGTCCTCCGCTTCCCGAGAGGTCCTCCGAGGTCCTCCGCTT 25920
OY 25921 CCGGAGAGGTCCTCCGCTTCCCGAGAGGTCCTCCGAGGTCCTCCGAGGTCCTCCGAGGTC 25980
Db 25921 CCGGAGAGGTCCTCCGCTTCCCGAGAGGTCCTCCGAGGTCCTCCGAGGTCCTCCGAGGTC 25980
OY 25981 CCGGAGGTCCTTCCCGAGAGGTCCTCCGAGGTCCTCCGAGGTCCTCCGAGGTCCTCC 26040
Db 25981 CCGGAGGTCCTTCCCGAGAGGTCCTCCGAGGTCCTCCGAGGTCCTCCGAGGTCCTCC 26040
OY 26041 CCGTTCCTCCGAGAGGTCCTCCGCTTCCCGAGAGGTCCTCCGAGGTCCTCCGCTTCCCG 26100
Db 26041 CCGTTCCTCCGAGAGGTCCTCCGCTTCCCGAGAGGTCCTCCGAGGTCCTCCGCTTCCCG 26100
OY 26101 AGGGTCCCGGCTTCCCGAGAGGTCCTCCGAGGTCCTCCGAGGTCCTCCGAGGTCCTCG 26160
Db 26101 AGGGTCCCGGCTTCCCGAGAGGTCCTCCGAGGTCCTCCGAGGTCCTCCGAGGTCCTCG 26160
OY 26161 GCTTCCCGTTTCCCGAGAGGTCCTCCGCTTCCCGAGAGGTCCTCCGAGGTCCTCCGCTT 26220
Db 26161 GCTTCCCGTTTCCCGAGAGGTCCTCCGCTTCCCGAGAGGTCCTCCGAGGTCCTCCGCTT 26220

QY 26221 CCCCCAGGCTCCCGGGCTCCCGTTCCCGAGGGTCCCGGGCTCCCGTTCCCGAGGGT 26280
DB 26221 CCCCCAGGCTCCCGGGCTCCCGTTCCCGAGGGTCCCGGGCTCCCGTTCCCGAGGGT 26280
QY 26281 CCGGGGCTCCCGTTCCCGAGGGTCCCGGGCTCCCGTTCCCGAGGGTCCCGGGCTCC 26340
DB 26281 CCGGGGCTCCCGTTCCCGAGGGTCCCGGGCTCCCGTTCCCGAGGGTCCCGGGCTCC 26340
QY 26341 CCGTTCCCGAGGGTCCCGGGCTCCCGTTCCCGAGGGTCCCGGGCTCCCGTTCCCGG 26400
DB 26341 CCGTTCCCGAGGGTCCCGGGCTCCCGTTCCCGAGGGTCCCGGGCTCCCGTTCCCGG 26400
QY 26401 AGGGTCCCGAGGGTCCCGTTCCCGAGGGTCCCGGGCTCCCGTTCCCGAGGGTCCCGG 26460
DB 26401 AGGGTCCCGAGGGTCCCGTTCCCGAGGGTCCCGGGCTCCCGTTCCCGAGGGTCCCGG 26460
QY 26461 GCTCCCGTTCCCGAGGGTCCCGGGCTCCCGTTCCCGAGGGTCCCGGGCTCCCGGTT 26520
DB 26461 GCTCCCGTTCCCGAGGGTCCCGGGCTCCCGTTCCCGAGGGTCCCGGGCTCCCGGTT 26520
QY 26521 CCGCGATTCAAGCTTAAAGTGTATTTAGCAAAACACAGTTTTCGCGGTTTGGG 26580
DB 26521 CCGCGATTCAAGCTTAAAGTGTATTTAGCAAAACACAGTTTTCGCGGTTTGGG 26580
QY 26581 TTGTACATACACGGGGGTGCGATTTGGCCCGCATGCAAAAATAACGTTGGTTTCC 26640
DB 26581 TTGTACATACACGGGGGTGCGCATTTGGCCCGCATGCAAAAATAACGTTGGTTTCC 26640
QY 26641 GAAACGCGTAGGCTCTTATGTTTTCATGSCAGCTTTTCTGTACAGGTTAGAGTGTAA 26700
DB 26641 GAAACGCGTAGGCTCTTATGTTTTCATGSCAGCTTTTCTGTACAGGTTAGAGTGTAA 26700
QY 26701 GTTTTGTGTAGCAATGCAACAGTAGCTGCGCTGACCGGAAAGGAAAGCACTTTTAA 26760
DB 26701 GTTTTGTGTAGCAATGCAACAGTAGCTGCGCTGACCGGAAAGGAAAGCACTTTTAA 26760
QY 26761 CCGCAGTGTACCGCGGTGCGCATACGTTTAAAGTGCACATGCGCGGTCCCGGCGTGG 26820
DB 26761 CCGCAGTGTACCGCGGTGCGCATACGTTTAAAGTGCACATGCGCGGTCCCGGCGTGG 26820
QY 26821 TACCTTAAAGTTTACGTTAGCAATTTAGCGGGCTGTTACAGGCCCTCCCGCCCTTGA 26880
DB 26821 TACCTTAAAGTTTACGTTAGCAATTTAGCGGGCTGTTACAGGCCCTCCCGCCCTTGA 26880
QY 26881 GGAAGAAATGAATTTCTTGGCAGTTGACGTTTATGCTATAGAGGGCATCTTCTTAA 26940
DB 26881 GGAAGAAATGAATTTCTTGGCAGTTGACGTTTATGCTATAGAGGGCATCTTCTTAA 26940
QY 26941 CTGTGGGTGCGGACGCGAGTACTTGCACATCCGTTTATAGCCCTATTAAAGATT 27000
DB 26941 CTGTGGGTGCGGACGCGAGTACTTGCACATCCGTTTATAGCCCTATTAAAGATT 27000
QY 27001 TATCAGGCGCTTCTCAAGACAGCGCTGCGCTGTAGAGAGGCTTTTGCCACACGA 27060
DB 27001 TATCAGGCGCTTCTCAAGACAGCGCTGCGCTGTAGAGAGGCTTTTGCCACACGA 27060
QY 27061 TTACCGGCTCTGGGGGACATAACGCCATAGGCCAAGAGTGTGCAAAATAACACGA 27120
DB 27061 TTACCGGCTCTGGGGGACATAACGCCATAGGCCAAGAGTGTGCAAAATAACACGA 27120
QY 27121 CGGACGCAACTGTGGGTGCGGTTTGGCGTGTGGGTGTTGGGTATGTAGTGA 27180
DB 27121 CGGACGCAACTGTGGGTGCGGTTTGGCGTGTGGGTGTTGGGTATGTAGTGA 27180
QY 27181 TAAAGTTAAAGACGACGAGCTTTTAAAGTGTGCGCATAGCCGTTCTACCGGTGACGC 27240
DB 27181 TAAAGTTAAAGACGACGAGCTTTTAAAGTGTGCGCATAGCCGTTCTACCGGTGACGC 27240
QY 27241 GTAGAGGCGGTGAGTCTCAGTGTCTGTTCACAGCGGCAATGGAGGAGACACAGAA 27300
DB 27241 GTAGAGGCGGTGAGTCTCAGTGTCTGTTCACAGCGGCAATGGAGGAGACACAGAA 27300

QY 27301 TTACTGAGCGGAATTAAGAGCATCGCCGCAACGCGAGAGACATGTTCTACGAGT 27360
DB 27301 TTACTGAGCGGAATTAAGAGCATCGCCGCAACGCGAGAGACATGTTCTACGAGT 27360
QY 27361 TCGGCTGTGTTCTTGGCGCTAGTGGCGCTTTTGGCATCAAGCGATTAAGTGTGCTTAA 27420
DB 27361 TCGGCTGTGTTCTTGGCGCTAGTGGCGCTTTTGGCATCAAGCGATTAAGTGTGCTTAA 27420
QY 27421 ACCGCGATTCCCGCACCCCTACCTTAAGTAGGCGATGTATATGAGACCAATAAACA 27480
DB 27421 ACCGCGATTCCCGCACCCCTACCTTAAGTAGGCGATGTATATGAGACCAATAAACA 27480
QY 27481 AAACAGCTAACGTTGATTTGTTGAACATTTTATTTAGAGAGTTCTTCGAGACA 27540
DB 27481 AAACAGCTAACGTTGATTTGTTGAACATTTTATTTAGAGAGTTCTTCGAGACA 27540
QY 27541 TTTTGTGTATGTGACACGGGGGCGGCTGTGGCTGTGCTCCACCGGGGCGCGCGG 27600
DB 27541 TTTTGTGTATGTGACACGGGGGCGGCTGTGGCTGTGCTCCACCGGGGCGCGCGG 27600
QY 27601 ACTGCGCATTTGATCGAGGGGCGGCAAGCGCCAGCGGGGGGCGAGAGCTGAA 27660
DB 27601 ACTGCGCATTTGATCGAGGGGCGGCAAGCGCCAGCGGGGGGCGAGAGCTGAA 27660
QY 27661 GAATGGCGTTTACATTAACAGATTCTTGGCGCGGCGGCGGTGAGTTGCCGCTGCTGG 27720
DB 27661 GAATGGCGTTTACATTAACAGATTCTTGGCGCGGCGGCGGTGAGTTGCCGCTGCTGG 27720
QY 27721 CGAGACGGCGTGTGCTGCGCGCTGCGGGGCGGTTGCGTTGCTGTGATGCCCT 27780
DB 27721 CGAGACGGCGTGTGCTGCGCGCTGCGGGGCGGTTGCGTTGCTGTGATGCCCT 27780
QY 27781 GCGGCTGTGTAGGCGCTGTGGGGGCGTGAAGTGGTGTCCGTTCCGGAATACACATCGG 27840
DB 27781 GCGGCTGTGTAGGCGCTGTGGGGGCGTGAAGTGGTGTCCGTTCCGGAATACACATCGG 27840
QY 27841 GCTGTACGCTTAGGTACCGGCGCACAGCGGTAGTGTGTGGCCACAGAACTGAACGGGCG 27900
DB 27841 GCTGTACGCTTAGGTACCGGCGCACAGCGGTAGTGTGTGGCCACAGAACTGAACGGGCG 27900
QY 27901 GTGGTGTGGGTGTGTGTGCGGCTGTGCGCGGAGAGTGTGGACCGCGGCTGTTTAA 27960
DB 27901 GTGGTGTGGGTGTGTGTGCGGCTGTGCGCGGAGAGTGTGGACCGCGGCTGTTTAA 27960
QY 27961 GGTCCCTAGATTCGCGCTGGAATGTCCAATATGTTTGGACAGCGCATGAGTCTTGT 28020
DB 27961 GGTCCCTAGATTCGCGCTGGAATGTCCAATATGTTTGGACAGCGCATGAGTCTTGT 28020
QY 28021 GTATGCCAGCTCTCGGCTGTGGAACACAGGGCTGTGGAAGCTCCACGTTCCGTTTGC 28080
DB 28021 GTATGCCAGCTCTCGGCTGTGGAACACAGGGCTGTGGAAGCTCCACGTTCCGTTTGC 28080
QY 28081 GCTTCTGTGTGCGAGACGCTGCGGAGCGTACGCTGTGAGGAAATGATACGTGGCGG 28140
DB 28081 GCTTCTGTGTGCGAGACGCTGCGGAGCGTACGCTGTGAGGAAATGATACGTGGCGG 28140
QY 28141 CATACGGAGAGGTTGGGGGCAACCGCGCATGGAAGGAAAGGAAAGGAGCGTGGCGGAGG 28200
DB 28141 CATACGGAGAGGTTGGGGGCAACCGCGCATGGAAGGAAAGGAAAGGAGCGTGGCGGAGG 28200
QY 28201 GTGGGTACGATGGGAGCTACGCTACGGCGCGGTATCCACAGATGATACCGCGCTTGG 28260
DB 28201 GTGGGTACGATGGGAGCTACGCTACGGCGCGGTATCCACAGATGATACCGCGCTTGG 28260
QY 28261 CCGGATGAGAGGTGGCGCAAAACGTTACGTGCGGTGGCCCTGGTTGGCATGTTATGCA 28320
DB 28261 CCGGATGAGAGGTGGCGCAAAACGTTACGTGCGGTGGCCCTGGTTGGCATGTTATGCA 28320
QY 28321 GACTGCTGTGACCATGTTGCAAAAGGTGCTTGGGGAATGTGATGTTGCTCCGAGGA 28380
DB 28321 GACTGCTGTGACCATGTTGCAAAAGGTGCTTGGGGAATGTGATGTTGCTCCGAGGA 28380
QY 28381 GGGCGCTCATGTTCCGGGTGTGCGGCTTACCGCAAGTGTGAGCGCAGGAAACTGGGCTTG 28440

```

Db      28381  |||
Qy      28441  CTTTAAATACGACTTTCGACACTTGGCCACGCTTATCTGTTTTCAGCAGCTTC 28500
Db      28441  CTTTAAATACGACTTTCGACACTTGGCCACGCTTATCTGTTTTCAGCAGCTTC 28500
Qy      28501  TCGGATCTCGGATTAATCCGGGCTCGATCCCTTGGCCATCACTGTCACAGAGGCCG 28560
Db      28501  TCGGATCTCGGATTAATCCGGGCTCGATCCCTTGGCCATCACTGTCACAGAGGCCG 28560
Qy      28561  CGAATCTGGGGGTGACCTGACGTTTGGCAAGATCTTAACAATTAACGCTATTTTAC 28620
Db      28561  CGAATCTGGGGGTGACCTGACGTTTGGCAAGATCTTAACAATTAACGCTATTTTAC 28620
Qy      28621  CGGCTTCCTCTCCGTAAGAAATCAAACTTGGAGACGACCATGTAGGCTCTGCTCCG 28680
Db      28621  CGGCTTCCTCTCCGTAAGAAATCAAACTTGGAGACGACCATGTAGGCTCTGCTCCG 28680
Qy      28681  AAACGGCGATTTACCCCTACGCTCCGCTCCGACAGACGACGCTGTAACGCGG 28740
Db      28681  AAACGGCGATTTACCCCTACGCTCCGCTCCGACAGACGACGCTGTAACGCGG 28740
Qy      28741  GTGGGTGATTTGGGGTCTTGGAGCTCTTGGGTGGAGGAGGAGGAGAGGCTCCGGG 28800
Db      28741  GTGGGTGATTTGGGGTCTTGGAGCTCTTGGGTGGAGGAGGAGGAGGAGGCTCCGGG 28800
Qy      28801  GCCATGTGTGTAACATCTCCACAGGAGGAGTCCAGAGCATGGGGTTTACGTGATCTGG 28860
Db      28801  GCCATGTGTGTAACATCTCCACAGGAGGAGTCCAGAGCATGGGGTTTACGTGATCTGG 28860
Qy      28861  CCGCTGCGGAGTCCCCCGGACGCGCTGACGCCACAGGCAAGAAATGCTGTTAGCT 28920
Db      28861  CCGCTGCGGAGTCCCCCGGACGCGCTGACGCCACAGGCAAGAAATGCTGTTAGCT 28920
Qy      28921  TGGCCAGGCAAAATATCCGCTGTGTTACTTGAAGAGACGATTTGCTGCTACAGGGG 28980
Db      28921  TGGCCAGGCAAAATATCCGCTGTGTTACTTGAAGAGACGATTTGCTGCTACAGGGG 28980
Qy      28981  CTTGCGGAGAGTCTCTATGTTTATCGGTAGAGGAGTCCGTATACGGGAGCAGGGTCCCA 29040
Db      28981  CTTGCGGAGAGTCTCTATGTTTATCGGTAGAGGAGTCCGTATACGGGAGCAGGGTCCCA 29040
Qy      29041  CGATTTAGAGGCTCTAAATACAGCTCTTTTCTATCTTTGTTAGCTGACCATCTCACT 29100
Db      29041  CGATTTAGAGGCTCTAAATACAGCTCTTTTCTATCTTTGTTAGCTGACCATCTCACT 29100
Qy      29101  ATCCCCCAACGTAACAGGAGTATGTGGGTGGGTGCTGCGTGAGACCCCAAGAGATGA 29160
Db      29101  ATCCCCCAACGTAACAGGAGTATGTGGGTGGGTGCTGCGTGAGACCCCAAGAGATGA 29160
Qy      29161  GCGCCGGCTCTTGGGGGCTGATGTGGGCGTTATCCGTTGTGAATTTAAATACGTTTC 29220
Db      29161  GCGCCGGCTCTTGGGGGCTGATGTGGGCGTTATCCGTTGTGAATTTAAATACGTTTC 29220
Qy      29221  TCCCTGGGAGCTCAGAGTTTCTTCACTGCTGCTGTGCGAAATGTACATAGGCTTGA 29280
Db      29221  TCCCTGGGAGCTCAGAGTTTCTTCACTGCTGCTGTGCGAAATGTACATAGGCTTGA 29280
Qy      29281  ACGTGTACCTTCTGAAGAGGCAATTGCAATACCGGACGAGGAGATATTGCTCTCG 29340
Db      29281  ACGTGTACCTTCTGAAGAGGCAATTGCAATACCGGACGAGGAGATATTGCTCTCG 29340
Qy      29341  GGGGTAAAGTTCCGTTGAGTTCTGAAAAATCGTTTACGATGGGTTAAAGAGATGGGG 29400
Db      29341  GGGGTAAAGTTCCGTTGAGTTCTGAAAAATCGTTTACGATGGGTTAAAGAGATGGGG 29400
Qy      29401  TTTTCTGACGCAAGTTGCTCTGAGAAACAAAAGGGGGGCTCTGTGGCTTTACTTCAACG 29460
Db      29401  TTTTCTGACGCAAGTTGCTCTGAGAAACAAAAGGGGGGCTCTGTGGCTTTACTTCAACG 29460
Qy      29461  GGGGTGCGGTGCTGTTTAAAGGTTAGGGACTACGTTTGTGCAACCTGGGGTTAAGCC 29520
Db      29461  GGGGTGCGGTGCTGTTTAAAGGTTAGGGACTACGTTTGTGCAACCTGGGGTTAAGCC 29520

```

```

Db      29461  GGGGTGCGGTGCTGTTTAAAGGTTAGGGACTACGTTTGTGCAACCTGGGGTTAAGCC 29520
Qy      29521  ACAGCGTACGCGTGTGTTCCGGAAAAACCTAACGAGTGGGAATTAATCTTAATACGCA 29580
Db      29521  ACAGCGTACGCGTGTGTTCCGGAAAAACCTAACGAGTGGGAATTAATCTTAATACGCA 29580
Qy      29581  GCGTCAATACCATGCTGCTGTTGGCAGTGAAGTACGTTTGGGCTTGGGGCAGC 29640
Db      29581  GCGTCAATACCATGCTGCTGTTGGCAGTGAAGTACGTTTGGGCTTGGGGCAGC 29640
Qy      29641  CTGACACAGAGCCCTGGGTGAGGTTGTTGGCGGCAAGATTTTATACGTAATTA 29700
Db      29641  CTGACACAGAGCCCTGGGTGAGGTTGTTGGCGGCAAGATTTTATACGTAATTA 29700
Qy      29701  TTTCCGGCCACATTAATGCAACGGAAGTCAATCTTGAACAGGTGGAGCTCCGGGTACG 29760
Db      29701  TTTCCGGCCACATTAATGCAACGGAAGTCAATCTTGAACAGGTGGAGCTCCGGGTACG 29760
Qy      29761  GTGGCTTCGTCGAGGAGTGTGCGGATGTTCCGGGATCCAGGAGTTCCGGGCTGGG 29820
Db      29761  GTGGCTTCGTCGAGGAGTGTGCGGATGTTCCGGGATCCAGGAGTTCCGGGCTGGG 29820
Qy      29821  ATTTTCCGTCGCGGCTCCGCGCTTAAAGTCTCAACAGACGACTATTGTTTCCGTCA 29880
Db      29821  ATTTTCCGTCGCGGCTCCGCGCTTAAAGTCTCAACAGACGACTATTGTTTCCGTCA 29880
Qy      29881  ATTAACAGCGTGTATGAGTCCGCTCAGCTACACACGCTGCGGACGCGGACGATCCAG 29940
Db      29881  ATTAACAGCGTGTATGAGTCCGCTCAGCTACACACGCTGCGGACGCGGACGATCCAG 29940
Qy      29941  GACCAAAAATAAATACCTGTCGTATGTCGTATGTCGTAATCCGAATTTGCTTCAATATATC 30000
Db      29941  GACCAAAAATAAATACCTGTCGTATGTCGTATGTCGTAATCCGAATTTGCTTCAATATATC 30000
Qy      30001  GTTGGCCAGACCGGGGGGAGTGGTGGCAAAAGATGGCGGACGAGCTTCTCCGCGCT 30060
Db      30001  GTTGGCCAGACCGGGGGGAGTGGTGGCAAAAGATGGCGGACGAGCTTCTCCGCGCT 30060
Qy      30061  TAAACGTAGCGAGCTTTGAGCTGAATCAAGCTGCCAGGCTCCCTAAGCTGATTTTG 30120
Db      30061  TAAACGTAGCGAGCTTTGAGCTGAATCAAGCTGCCAGGCTCCCTAAGCTGATTTTG 30120
Qy      30121  GTTCAGAGTGTCAAAATTTCTTAATCTGTAATCTGGAACCGGTGAGGTTACGACGAGAGT 30180
Db      30121  GTTCAGAGTGTCAAAATTTCTTAATCTGTAATCTGGAACCGGTGAGGTTACGACGAGAGT 30180
Qy      30181  GTGTTTAAATGAGATATGAGCTTTGCTTCCACAGCGCGCTAGATACGACCCGGAAACA 30240
Db      30181  GTGTTTAAATGAGATATGAGCTTTGCTTCCACAGCGCGCTAGATACGACCCGGAAACA 30240
Qy      30241  AAACGACGTGGGGGCTGTGGCGCGCGCAAAATTTGGGAATTTATTTCTGTCAG 30300
Db      30241  AAACGACGTGGGGGCTGTGGCGCGCGCAAAATTTGGGAATTTATTTCTGTCAG 30300
Qy      30301  GAAATCAAAAAGTTGTCCTTTTAAAGTATTTTGAACCGGAGCGGCTCTCACTT 30360
Db      30301  GAAATCAAAAAGTTGTCCTTTTAAAGTATTTTGAACCGGAGCGGCTCTCACTT 30360
Qy      30361  GGAATAATCTCCACCCAGGACGAGGCTGAGGCGCGGCTGAGGCGGATCTGGGTGT 30420
Db      30361  GGAATAATCTCCACCCAGGACGAGGCTGAGGCGCGGCTGAGGCGGATCTGGGTGT 30420
Qy      30421  GATTGGGCCAGCTCCATATGACAGCTTAACCAAACTTAACAGCTTATGTCGAGAGGCC 30480
Db      30421  GATTGGGCCAGCTCCATATGACAGCTTAACCAAACTTAACAGCTTATGTCGAGAGGCC 30480
Qy      30481  GGTTCGAGGTTCCATTTGAGCTTGAAGGAGGACAGCTTCCGCTGAACAAATGTGT 30540
Db      30481  GGTTCGAGGTTCCATTTGAGCTTGAAGGAGGACAGCTTCCGCTGAACAAATGTGT 30540
Qy      30541  GCGAAGAGTATATACAGATCTGTGCTCAGGTGGCTACCGGATCCGCGGCTTCTGGAAC 30600
Db      30541  GCGAAGAGTATATACAGATCTGTGCTCAGGTGGCTACCGGATCCGCGGCTTCTGGAAC 30600

```

QY 30601 GGGTAGACAGTCCGCTGTGTCACGCGGTATATCAGCTGGTTGTAAAGATCCGC 30660
|||||
Db 30601 GGGTAGACAGTCCGCTGTGTCACGCGGTATATCAGCTGGTTGTAAAGATCCGC 30660
QY 30661 GTTGTACTTGTGTTTGTGTTTAAAGGCGCTAGAGAGCGCTGTGCTCGATTCGAATA 30720
30661 GTTGTACTTGTGTTTGTGTTTAAAGGCGCTAGAGAGCGCTGTGCTCGATTCGAATA 30720
Db 30721 TGTAACTGGAACCCAGGCGCTGTGTTTGTAGTGAAGACAAAGCTGCCAG 30780
30721 TGTAACTGGAACCCAGGCGCTGTGTTTGTAGTGAAGACAAAGCTGCCAG 30780
QY 30781 CTTTGTCCGAGGTATACCAAGGCGCTTTCAGTTGGCGCAACGGGGTACCTGCGC 30840
30781 CTTTGTCCGAGGTATACCAAGGCGCTTTCAGTTGGCGCAACGGGGTACCTGCGC 30840
Db 30781 CTTTGTCCGAGGTATACCAAGGCGCTTTCAGTTGGCGCAACGGGGTACCTGCGC 30840
QY 30841 GTGACAGTAGTACCGCTTGAGAGGACAGCGCGGCTGCTCGATTCGTTGCGGAC 30900
30841 GTGACAGTAGTACCGCTTGAGAGGACAGCGCGGCTGCTCGATTCGTTGCGGAC 30900
Db 30841 GTGACAGTAGTACCGCTTGAGAGGACAGCGCGGCTGCTCGATTCGTTGCGGAC 30900
QY 30901 ATCCGGTAAAGTCTTGTGTATCGAGCGGCTGTGAGATTACGGACAGATTAGCTT 30960
30901 ATCCGGTAAAGTCTTGTGTATCGAGCGGCTGTGAGATTACGGACAGATTAGCTT 30960
Db 30901 ATCCGGTAAAGTCTTGTGTATCGAGCGGCTGTGAGATTACGGACAGATTAGCTT 30960
QY 30961 TAGAGACGTGAGATTGTTGAAGTTGTGCTCCGCAATCTGTGGGAACACCTGCG 31020
30961 TAGAGACGTGAGATTGTTGAAGTTGTGCTCCGCAATCTGTGGGAACACCTGCG 31020
Db 30961 TAGAGACGTGAGATTGTTGAAGTTGTGCTCCGCAATCTGTGGGAACACCTGCG 31020
QY 31021 TTGCATAGCGGTTATCTGTAGAGCTACTGACAGGCGCTATTTGTGGACCATTTGTT 31080
31021 TTGCATAGCGGTTATCTGTAGAGCTACTGACAGGCGCTATTTGTGGACCATTTGTT 31080
Db 31021 TTGCATAGCGGTTATCTGTAGAGCTACTGACAGGCGCTATTTGTGGACCATTTGTT 31080
QY 31081 TTGGTTCATAGTACAGCTTGGGAGAGCTCCAGACGGAGATCCTGGTTTACCTGTAATC 31140
31081 TTGGTTCATAGTACAGCTTGGGAGAGCTCCAGACGGAGATCCTGGTTTACCTGTAATC 31140
Db 31081 TTGGTTCATAGTACAGCTTGGGAGAGCTCCAGACGGAGATCCTGGTTTACCTGTAATC 31140
QY 31141 CGGGTCCCGGGGCTATTGTGACAAAGAAAGCGTCTCATGTGTCTGCGGGGCGATTTT 31200
31141 CGGGTCCCGGGGCTATTGTGACAAAGAAAGCGTCTCATGTGTCTGCGGGGCGATTTT 31200
Db 31141 CGGGTCCCGGGGCTATTGTGACAAAGAAAGCGTCTCATGTGTCTGCGGGGCGATTTT 31200
QY 31201 GGGTTCGCGGTTAGTAGATTTGGGCAATGGCGGTTTCCCTCCCGGGAGCGAGATC 31260
31201 GGGTTCGCGGTTAGTAGATTTGGGCAATGGCGGTTTCCCTCCCGGGAGCGAGATC 31260
Db 31201 GGGTTCGCGGTTAGTAGATTTGGGCAATGGCGGTTTCCCTCCCGGGAGCGAGATC 31260
QY 31261 CCGGACCATGTTTGTGATTGTTCTAGTGGCGCATGACCACTTCTCCGTTGGTGTG 31320
31261 CCGGACCATGTTTGTGATTGTTCTAGTGGCGCATGACCACTTCTCCGTTGGTGTG 31320
Db 31261 CCGGACCATGTTTGTGATTGTTCTAGTGGCGCATGACCACTTCTCCGTTGGTGTG 31320
QY 31321 CGTTTGCAGACGTTGTCTAGTTCTAGCCGAGACAGTTTTCGACAGCGTGTGAACCTT 31380
31321 CGTTTGCAGACGTTGTCTAGTTCTAGCCGAGACAGTTTTCGACAGCGTGTGAACCTT 31380
Db 31321 CGTTTGCAGACGTTGTCTAGTTCTAGCCGAGACAGTTTTCGACAGCGTGTGAACCTT 31380
QY 31381 TACGCCACGCTGTTGATTTGCGATCACAACGCGTTTCTTCTTATCTAGAGATG 31440
31381 TACGCCACGCTGTTGATTTGCGATCACAACGCGTTTCTTCTTATCTAGAGATG 31440
Db 31381 TACGCCACGCTGTTGATTTGCGATCACAACGCGTTTCTTCTTATCTAGAGATG 31440
QY 31441 TTTGTGAATTAAGACAGATTTGTTGGATGGGGGCCAAAAGTTGCGGTAATTGGCCG 31500
31441 TTTGTGAATTAAGACAGATTTGTTGGATGGGGGCCAAAAGTTGCGGTAATTGGCCG 31500
Db 31441 TTTGTGAATTAAGACAGATTTGTTGGATGGGGGCCAAAAGTTGCGGTAATTGGCCG 31500
QY 31501 CCGTGGTTTTCTGGGATCTCATACAGCATTTTTCGACGTGCGCATCTTCCCATTTGGC 31560
31501 CCGTGGTTTTCTGGGATCTCATACAGCATTTTTCGACGTGCGCATCTTCCCATTTGGC 31560
Db 31501 CCGTGGTTTTCTGGGATCTCATACAGCATTTTTCGACGTGCGCATCTTCCCATTTGGC 31560
QY 31561 TAAAAAACCCGTTAAGCGCGCGAGCTGTTGATTAATGTAGAGGCAAGCGCTGATG 31620
31561 TAAAAAACCCGTTAAGCGCGCGAGCTGTTGATTAATGTAGAGGCAAGCGCTGATG 31620
Db 31561 TAAAAAACCCGTTAAGCGCGCGAGCTGTTGATTAATGTAGAGGCAAGCGCTGATG 31620
QY 31621 ACTCAGATGATTTGTTTAAAGTGTGTTTCTGTTCTTAATAGAGGCAAGGCGCTTACCG 31680
31621 ACTCAGATGATTTGTTTAAAGTGTGTTTCTGTTCTTAATAGAGGCAAGGCGCTTACCG 31680
Db 31621 ACTCAGATGATTTGTTTAAAGTGTGTTTCTGTTCTTAATAGAGGCAAGGCGCTTACCG 31680

QY 31681 ACCAGTTTTCGTCCTCTTGGCGGCGCTCTGCCATATATGCCAGGAATCTGTACGTT 31740
|||||
Db 31681 ACCAGTTTTCGTCCTCTTGGCGGCGCTCTGCCATATATGCCAGGAATCTGTACGTT 31740
QY 31741 GGTGTAAAGCCCTGCCATTCGCTGTGATATTTTATTCGTTGCGGGAATACAGCCGCG 31800
31741 GGTGTAAAGCCCTGCCATTCGCTGTGATATTTTATTCGTTGCGGGAATACAGCCGCG 31800
Db 31741 GGTGTAAAGCCCTGCCATTCGCTGTGATATTTTATTCGTTGCGGGAATACAGCCGCG 31800
QY 31801 TTAGGACGCTGAGTTGCAATATAGACAGCTTTTGTGATGTTGCTATTAACGGTAA 31860
31801 TTAGGACGCTGAGTTGCAATATAGACAGCTTTTGTGATGTTGCTATTAACGGTAA 31860
Db 31801 TTAGGACGCTGAGTTGCAATATAGACAGCTTTTGTGATGTTGCTATTAACGGTAA 31860
QY 31861 GCACAAATCTGCTATTCGCTACTAGGGAACCTCGAAAAATCTTAATTTAACT 31920
31861 GCACAAATCTGCTATTCGCTACTAGGGAACCTCGAAAAATCTTAATTTAACT 31920
Db 31861 GCACAAATCTGCTATTCGCTACTAGGGAACCTCGAAAAATCTTAATTTAACT 31920
QY 31921 TTTTGGTTCCTGAGCTGTTGGGCAATTAAGAAACCTTAAATATCATCAAGGAC 31980
31921 TTTTGGTTCCTGAGCTGTTGGGCAATTAAGAAACCTTAAATATCATCAAGGAC 31980
Db 31921 TTTTGGTTCCTGAGCTGTTGGGCAATTAAGAAACCTTAAATATCATCAAGGAC 31980
QY 31981 GGTGTTGATTAACCGTCCGCTATACGTAGTAAAGTGGGCGGAGTTCCAGCCGTTGGGTG 32040
31981 GGTGTTGATTAACCGTCCGCTATACGTAGTAAAGTGGGCGGAGTTCCAGCCGTTGGGTG 32040
Db 31981 GGTGTTGATTAACCGTCCGCTATACGTAGTAAAGTGGGCGGAGTTCCAGCCGTTGGGTG 32040
QY 32041 AGGCGGAAAGGCGCTTGAGAGGTCGACAGCTGCTTACATTTGTAATGCAACCGCATGGCG 32100
32041 AGGCGGAAAGGCGCTTGAGAGGTCGACAGCTGCTTACATTTGTAATGCAACCGCATGGCG 32100
Db 32041 AGGCGGAAAGGCGCTTGAGAGGTCGACAGCTGCTTACATTTGTAATGCAACCGCATGGCG 32100
QY 32101 AAGGAGGCTGCTGCTTGGCGAGCTTGTCCGTCAGATGCGGATCGGAACCTTAGAT 32160
32101 AAGGAGGCTGCTGCTTGGCGAGCTTGTCCGTCAGATGCGGATCGGAACCTTAGAT 32160
Db 32101 AAGGAGGCTGCTGCTTGGCGAGCTTGTCCGTCAGATGCGGATCGGAACCTTAGAT 32160
QY 32161 GGGACGAGTCTCCGAGATACGTAGCTTTGACACCCGAAACACCGATCTTGAATG 32220
32161 GGGACGAGTCTCCGAGATACGTAGCTTTGACACCCGAAACACCGATCTTGAATG 32220
Db 32161 GGGACGAGTCTCCGAGATACGTAGCTTTGACACCCGAAACACCGATCTTGAATG 32220
QY 32221 ATGATGTGTTCCCGTGTGATAGTACGACGCGCTTAAATGAGCCCTGGAAGTCAAACTATG 32280
32221 ATGATGTGTTCCCGTGTGATAGTACGACGCGCTTAAATGAGCCCTGGAAGTCAAACTATG 32280
Db 32221 ATGATGTGTTCCCGTGTGATAGTACGACGCGCTTAAATGAGCCCTGGAAGTCAAACTATG 32280
QY 32281 ACCTACCCACGTTCCGTCGGAAGCCGCGGAAATTAACGACCCGAGCGCTGTATG 32340
32281 ACCTACCCACGTTCCGTCGGAAGCCGCGGAAATTAACGACCCGAGCGCTGTATG 32340
Db 32281 ACCTACCCACGTTCCGTCGGAAGCCGCGGAAATTAACGACCCGAGCGCTGTATG 32340
QY 32341 CACATCCGAGTCCCGGCTTAAAGGCGGTTGTCGCGGCGGTCGCGGCTGCCAAG 32400
32341 CACATCCGAGTCCCGGCTTAAAGGCGGTTGTCGCGGCGGTCGCGGCTGCCAAG 32400
Db 32341 CACATCCGAGTCCCGGCTTAAAGGCGGTTGTCGCGGCGGTCGCGGCTGCCAAG 32400
QY 32401 TGTCCGCTTCTCGGCTAGACTTCAATATGTTGAGACAGAGTTTGGGATAGAGAGA 32460
32401 TGTCCGCTTCTCGGCTAGACTTCAATATGTTGAGACAGAGTTTGGGATAGAGAGA 32460
Db 32401 TGTCCGCTTCTCGGCTAGACTTCAATATGTTGAGACAGAGTTTGGGATAGAGAGA 32460
QY 32461 CCGCGGAGCTTACCAGGCTCAATTTTCTCCGAGACCGACGAATATGCCGAATATC 32520
32461 CCGCGGAGCTTACCAGGCTCAATTTTCTCCGAGACCGACGAATATGCCGAATATC 32520
Db 32461 CCGCGGAGCTTACCAGGCTCAATTTTCTCCGAGACCGACGAATATGCCGAATATC 32520
QY 32521 CCGAGGCTACTACTACAGCGCCGCTTGAAGGCGGTGACAGAAATTTTACCTCGCGG 32580
32521 CCGAGGCTACTACTACAGCGCCGCTTGAAGGCGGTGACAGAAATTTTACCTCGCGG 32580
Db 32521 CCGAGGCTACTACTACAGCGCCGCTTGAAGGCGGTGACAGAAATTTTACCTCGCGG 32580
QY 32581 GTAGGGGTGCAATCTCGGAGCCTGTCGACAAACCTAGTCAAGGTGGGGTTAAAC 32640
32581 GTAGGGGTGCAATCTCGGAGCCTGTCGACAAACCTAGTCAAGGTGGGGTTAAAC 32640
Db 32581 GTAGGGGTGCAATCTCGGAGCCTGTCGACAAACCTAGTCAAGGTGGGGTTAAAC 32640
QY 32641 GTAAAGCTAAAGCTGCTGAGTGTATTTTAAACTTGTGCGGATTAAGAGAGATG 32700
32641 GTAAAGCTAAAGCTGCTGAGTGTATTTTAAACTTGTGCGGATTAAGAGAGATG 32700
Db 32641 GTAAAGCTAAAGCTGCTGAGTGTATTTTAAACTTGTGCGGATTAAGAGAGATG 32700
QY 32701 ATGCTAAGGTTGATTAACCGAGCGGTTACCGTCCGCTTCAATCTCATCAGCCGATC 32760
32701 ATGCTAAGGTTGATTAACCGAGCGGTTACCGTCCGCTTCAATCTCATCAGCCGATC 32760
Db 32701 ATGCTAAGGTTGATTAACCGAGCGGTTACCGTCCGCTTCAATCTCATCAGCCGATC 32760
QY 32761 CTATGACGGAATATAGAAATGCTTTTAACTATCTAGAGGGGCTCATGGGTGGAA 32820

|||||
Db 32761 CTAATGCGAATATAGAAATGCCCTTTTATCTATCTATAGAGGGGCTCATGGGTTGGAA 32820
|||
Qy 32821 AAACAACGCTATTTGAATTCATGACTGGCATGGTGCCGAGGAAAAAGCTTTAAAGCTGTC 32880
|||||
Db 32821 AAAACAACGCTATTTGAATTCATGACTGGCATGGTGCCGAGGAAAAAGCTTTAAAGCTGTC 32880
|||
Qy 32881 CCGAGCCCATGAAATTTTGGAGCTGCTGTTATTTCAATATTCCTTTAAAGAACGCGGAGCA 32940
|||||
Db 32881 CCGAGCCCATGAAATTTTGGAGCTGCTGTTATTTCAATATTCCTTTAAAGAACGCGGAGCA 32940
|||
Qy 32941 TAGTTAAGCAAGGACCCACGGGAAATTTGATCACTTCTGCGCGATACGGGTGTCACA 33000
|||||
Db 32941 TAGTTAAGCAAGGACCCACGGGAAATTTGATCACTTCTGCGCGATACGGGTGTCACA 33000
|||
Qy 33001 GCAAGTTTGGCTACCGTTTCTGTCGACAGCCGCGGCATCGGTGCAACCTGCAACCGT 33060
|||||
Db 33001 GCAAGTTTGGCTACCGTTTCTGTCGACAGCCGCGGCATCGGTGCAACCTGCAACCGT 33060
|||
Qy 33061 GGCTGGTGGGAAACGGTACACAAAGCCAGCAATTTGATTTGTTTACACACACTAC 33120
|||||
Db 33061 GGCTGGTGGGAAACGGTACACAAAGCCAGCAATTTGATTTGTTTACACACACTAC 33120
|||
Qy 33121 TGTCCGCAACGGTGGTTTTCCGTGCTGTCACGTAAGTACAAAGCGCTAACGCCGATC 33180
|||||
Db 33121 TGTCCGCAACGGTGGTTTTCCGTGCTGTCACGTAAGTACAAAGCGCTAACGCCGATC 33180
|||
Qy 33181 ATCTGTTTCAAAATCTATCTCTTTCTCGGACACAGCGCGCATGTGTCGTTTGTCTAA 33240
|||||
Db 33181 ATCTGTTTCAAAATCTATCTCTTTCTCGGACACAGCGCGCATGTGTCGTTTGTCTAA 33240
|||
Qy 33241 GCCTCAACGTTTCGAGGCGGACAGCGCATTCACAAAGTGAAGCCGCTAAGGAAAGAAAG 33300
|||||
Db 33241 GCCTCAACGTTTCGAGGCGGACAGCGCATTCACAAAGTGAAGCCGCTAAGGAAAGAAAG 33300
|||
Qy 33301 GAATCAGCGAAACTACTGTCGACAGAGTAGCTGGGCGTACCATCGCGTCTCTGACT 33360
|||||
Db 33301 GAATCAGCGAAACTACTGTCGACAGAGTAGCTGGGCGTACCATCGCGTCTCTGACT 33360
|||
Qy 33361 GGGTATGATGCAATATCTCACACCGGAGCAAAATGTTTCAAGCTGTGTACAACTGTGT 33420
|||||
Db 33361 GGGTATGATGCAATATCTCACACCGGAGCAAAATGTTTCAAGCTGTGTGTGTGTGTGT 33420
|||
Qy 33421 CCATAGAGACATATGACATATGATTCAGATTCAGTTCAGTTCATACCCCTAACAA 33480
|||||
Db 33421 CCATAGAGACATATGACATATGATTCAGATTCAGTTCAGTTCATACCCCTAACAA 33480
|||
Qy 33481 AACTACATGAACAGAGTATGATACCATGCTGGCAGAAATGTTAGTATCGTTTAAAGAAC 33540
|||||
Db 33481 AACTACATGAACAGAGTATGATACCATGCTGGCAGAAATGTTAGTATCGTTTAAAGAAC 33540
|||
Qy 33541 ACGTACCTTATATGAGAGTCTGTTGGGACTTTTAAAGAGCTACGAAAGCTTCAAAATTT 33600
|||||
Db 33541 ACGTACCTTATATGAGAGTCTGTTGGGACTTTTAAAGAGCTACGAAAGCTTCAAAATTT 33600
|||
Qy 33601 TAAATGTTGACGAGAGACATATGATGATGCTGAGGCTCGGGGAAATATTTATG 33660
|||||
Db 33601 TAAATGTTGACGAGAGACATATGATGATGCTGAGGCTCGGGGAAATATTTATG 33660
|||
Qy 33661 GGCAGAGTATGCAATGAGCTATTTAAACGACGAGTAACTGGCAGCTCTTGGAA 33720
|||||
Db 33661 GGCAGAGTATGCAATGAGCTATTTAAACGACGAGTAACTGGCAGCTCTTGGAA 33720
|||
Qy 33721 GCTATATTCAAACGCTAACCAATTTGAAAGCAATGCGCGCTATTTAGTTTATATTTT 33780
|||||
Db 33721 GCTATATTCAAACGCTAACCAATTTGAAAGCAATGCGCGCTATTTAGTTTATATTTT 33780
|||
Qy 33781 TTTTCTATATTAAGGTTTCTGTAACGAGCAAAATTCGCTATGATGAAATTCAAATGTA 33840
|||||
Db 33781 TTTTCTATATTAAGGTTTCTGTAACGAGCAAAATTCGCTATGATGAAATTCAAATGTA 33840
|||
Qy 33841 GAGTTGAATTTAATGAAACATTTACCAATTAATTTGAGAAACGTAAAGCAATTA 33900
|||||

|||||
Db 33841 GAGTTGAATTTAATGAAACATTTACCAATTAATTTGAGAAACGTAAAGCAAAATTA 33900
|||||
Qy 33901 ACATCTATTTGTAATGGAAGATGCGGTGATACGATTCCTTACTGCTGGAACCAATGCTGTG 33960
|||||
Db 33901 ACATCTATTTGTAATGGAAGATGCGGTGATACGATTCCTTACTGCTGGAACCAATGCTGTG 33960
|||
Qy 33961 ACTTTGGAAAAAAGAAAGTTTGTGCGATCAAGTATATGTTAATGTGCTAATATATGAC 34020
|||||
Db 33961 ACTTTGGAAAAAAGAAAGTTTGTGCGATCAAGTATATGTTAATGTGCTAATATATGAC 34020
|||
Qy 34021 TATACATTTTGAATTCCTTCAAGTACCATGATTAATTAACCTTACGGTGAATTTAATAC 34080
|||||
Db 34021 TATACATTTTGAATTCCTTCAAGTACCATGATTAATTAACCTTACGGTGAATTTAATAC 34080
|||
Qy 34081 AGTTCTTTGCCAGTTTTTACTGGGAATTTTAAATGTAATGACACATGCTTTTAAACAGAGC 34140
|||||
Db 34081 AGTTCTTTGCCAGTTTTTACTGGGAATTTTAAATGTAATGTAATGACACATGCTTTTAAACAGAGC 34140
|||
Qy 34141 GTTTTATTTACGAAACGTAATTTATTTACCACTCAACAAACATTTAGATCTTTTATAC 34200
|||||
Db 34141 GTTTTATTTACGAAACGTAATTTATTTACCACTCAACAAACATTTAGATCTTTTATAC 34200
|||
Qy 34201 GCGGAAAAAATTAATGCAAGAAATGTTCAAGATTAATTTGATTTTCCAAATGTAATTAAT 34260
|||||
Db 34201 GCGGAAAAAATTAATGCAAGAAATGTTCAAGATTAATTTGATTTTCCAAATGTAATTAAT 34260
|||
Qy 34261 TCCGCAATTTATTAACGAAAAATTTGATATTAATGATATGATACCAATTAATTAATTAATCA 34320
|||||
Db 34261 TCCGCAATTTATTAACGAAAAATTTGATATTAATGATATGATACCAATTAATTAATTAATCA 34320
|||
Qy 34321 AATATGCAATGTTGTGCACTGTTTGTGTTGTTGTTCTTACACATTTCCAGGCTTAAAGGC 34380
|||||
Db 34321 AATATGCAATGTTGTGCACTGTTTGTGTTGTTGTTCTTACACATTTCCAGGCTTAAAGGC 34380
|||
Qy 34381 TATGATCTTATACGATTTATGCTTAAATTAATTAATTAATTAATTAATTAATTAATTAAT 34440
|||||
Db 34381 TATGATCTTATACGATTTATGCTTAAATTAATTAATTAATTAATTAATTAATTAATTAAT 34440
|||
Qy 34441 GCGCGAAATCTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 34500
|||||
Db 34441 GCGCGAAATCTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 34500
|||
Qy 34501 TTTGTTAGTTATGATAGTACCGCTTAAATGATTAATTAATTAATTAATTAATTAATTAAT 34560
|||||
Db 34501 TTTGTTAGTTATGATAGTACCGCTTAAATGATTAATTAATTAATTAATTAATTAATTAAT 34560
|||
Qy 34561 GCTATTTGAAGCAAAAGGCTGCTGCAAAATCCTTCAAAATGAAATGATATCTTATCTTTC 34620
|||||
Db 34561 GCTATTTGAAGCAAAAGGCTGCTGCAAAATCCTTCAAAATGAAATGATATCTTATCTTTC 34620
|||
Qy 34621 TTTTGTGAAGTTACTGCACTAATTTTATTTATTAATTAATTAATTAATTAATTAATTAAT 34680
|||||
Db 34621 TTTTGTGAAGTTACTGCACTAATTTTATTTATTAATTAATTAATTAATTAATTAATTAAT 34680
|||
Qy 34681 GTTAAAGTTGGGTGTTGTAACGGCATGTCAGGCTTAAAGGTTAATGATTAATTAATTAAT 34740
|||||
Db 34681 GTTAAAGTTGGGTGTTGTAACGGCATGTCAGGCTTAAAGGTTAATGATTAATTAATTAAT 34740
|||
Qy 34741 AGGCTGCTACCCCAACCTTAAATTTATGATGCTTAAATTTGAAAGCTTGTCCATATTT 34800
|||||
Db 34741 AGGCTGCTACCCCAACCTTAAATTTATGATGCTTAAATTTGAAAGCTTGTCCATATTT 34800
|||
Qy 34801 GCAAGAGTCCAGGTTTTTAACTCCGCAAAATGCAATGATATGATGATTAATTAATTAAT 34860
|||||
Db 34801 GCAAGAGTCCAGGTTTTTAACTCCGCAAAATGCAATGATATGATGATTAATTAATTAATTAAT 34860
|||
Qy 34861 CAAGAGGCTATTTTCAATGTTTAAATTTGATTAATTAATTAATTAATTAATTAATTAATTAAT 34920
|||||
Db 34861 CAAGAGGCTATTTTCAATGTTTAAATTTGATTAATTAATTAATTAATTAATTAATTAATTAAT 34920
|||
Qy 34921 ATTCTTAAACGAATTTGATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 34980
|||||
Db 34921 ATTCTTAAACGAATTTGATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 34980
|||

QY 34981 CAGCTAACCAACATTTAGGGGAATGTAAATGACATGATGAAGTTTAAACAACATT 35040
|||||
Db 34981 CAGCTAACCAACATTTAGGGGAATGTAAATGACATGATGAAGTTTAAACAACATT 35040
QY 35041 AAATTAAGCATGACAGATTCCTGCTGTTTATCCGTATATATGTTTCACATCATGTGT 35100
|||||
Db 35041 AAATTAAGCATGACAGATTCCTGCTGTTTATCCGTATATATGTTTCACATCATGTGT 35100
QY 35101 AATTAATGTAGATATATCATATATGATTAATCAAAATAGCAAAAGCCCATGACATCACATA 35160
|||||
Db 35101 AATTAATGTAGATATATCATATATGATTAATCAAAATAGCAAAAGCCCATGACATCACATA 35160
QY 35161 TTTCGGGTGTTTCCGCTGTTTATTAAGCTTAAGCTTGAATTTAGTAAACAAGCTA 35220
|||||
Db 35161 TTTCGGGTGTTTCCGCTGTTTATTAAGCTTAAGCTTGAATTTAGTAAACAAGCTA 35220
QY 35221 CGATCCGACGACCGACGACGTCMAAAGAACCGGCTCGAATGSCACAAAGAGCGTCT 35280
|||||
Db 35221 CGATCCGACGACCGACGACGTCMAAAGAACCGGCTCGAATGSCACAAAGAGCGTCT 35280
QY 35281 GGTTTTGGGCGCTGTGTGACGCTTTTACGCCACGCTATTAACGAGTTTTCAGTCATA 35340
|||||
Db 35281 GGTTTTGGGCGCTGTGTGACGCTTTTACGCCACGCTATTAACGAGTTTTCAGTCATA 35340
QY 35341 AATTTGACAGCGCTGGCATGGAAGCAAGTAACCGCGCTGATGCGCTTACGACATCACG 35400
|||||
Db 35341 AATTTGACAGCGCTGGCATGGAAGCAAGTAACCGCGCTGATGCGCTTACGACATCACG 35400
QY 35401 TACGTCATTAAGCTCCGTGCGCCCTGATACGCTCGGCTTACGAGGTTTCGAGGTTTC 35460
|||||
Db 35401 TACGTCATTAAGCTCCGTGCGCCCTGATACGCTCGGCTTACGAGGTTTCGAGGTTTC 35460
QY 35461 CTTAAAGGCGCATGTTTGTCTGCGGCGCTTATCCAAATGTCTCATTTTACCGGCC 35520
|||||
Db 35461 CTTAAAGGCGCATGTTTGTCTGCGGCGCTTATCCAAATGTCTCATTTTACCGGCC 35520
QY 35521 GGTACCGCCCTACACATTCGATATTTGATTAACCTTTTCGCCCGCAGATAGAGATTCGG 35580
|||||
Db 35521 GGTACCGCCCTACACATTCGATATTTGATTAACCTTTTCGCCCGCAGATAGAGATTCGG 35580
QY 35581 CTGTGTGATTCGATTTGTTTGAAGCTATGATGAGAACGAGGACTACAGACATGATGTAC 35640
|||||
Db 35581 CTGTGTGATTCGATTTGTTTGAAGCTATGATGAGAACGAGGACTACAGACATGATGTAC 35640
QY 35641 GGTGCAAAOCCCACTTCAAGCAACGCTTTCCCGATTCCTCTTGTGCAAC 35700
|||||
Db 35641 GGTGCAAAOCCCACTTCAAGCAACGCTTTCCCGATTCCTCTTGTGCAAC 35700
QY 35701 GATTAATTTTCATTCATTTATTTGTTTGAATGATTAAGCAACGATACGTTGTGAATTCGG 35760
|||||
Db 35701 GATTAATTTTCATTCATTTATTTGTTTGAATGATTAAGCAACGATACGTTGTGAATTCGG 35760
QY 35761 GATTTGTACAGAAGACACGACCTCATGCTATGATTAAGTATTTCTTTTATTTGAACA 35820
|||||
Db 35761 GATTTGTACAGAAGACACGACCTCATGCTATGATTAAGTATTTCTTTTATTTGAACA 35820
QY 35821 AATGTCGCTCTGATTTCTGTTTGAAGCTTTTCACTCTGCGCAAACTGTTAATAA 35880
|||||
Db 35821 AATGTCGCTCTGATTTCTGTTTGAAGCTTTTCACTCTGCGCAAACTGTTAATAA 35880
QY 35881 GCGTAAACCTTTAAAGTTGTTTCCGTTTCTTTTGTGATGATTAAGCGGGAGACGAGA 35940
|||||
Db 35881 GCGTAAACCTTTAAAGTTGTTTCCGTTTCTTTTGTGATGATTAAGCGGGAGACGAGA 35940
QY 35941 TTAGCGAGAACCTCGGATAGAGCGTGCCTGACATATTGATTCAATCACCTCTGCGCA 36000
|||||
Db 35941 TTAGCGAGAACCTCGGATAGAGCGTGCCTGACATATTGATTCAATCACCTCTGCGCA 36000
QY 36001 ACTTGAATGCCGACGCTCTGATTTTGGGAGGAAATTAATAATTTTGTGCGCG 36060
|||||
Db 36001 ACTTGAATGCCGACGCTCTGATTTTGGGAGGAAATTAATAATTTTGTGCGCG 36060

QY 36061 GTTAATATTCGCTGCGGACCGCGCAAAACCTGAAATTCCTTGAAGTGTGAGAC 36120
|||||
Db 36061 GTTAATATTCGCTGCGGACCGCGCAAAACCTGAAATTCCTTGAAGTGTGAGAC 36120
QY 36121 TCTATGAGATTTAAACAAAACACCATGTCTTCCAGCGCTGTTTACGCGGAGACATG 36180
|||||
Db 36121 TCTATGAGATTTAAACAAAACACCATGTCTTCCAGCGCTGTTTACGCGGAGACATG 36180
QY 36181 GATTCGAATATTCCTGATTAACGAGGCGCGCGCTTACGATTAATTCGATTAACAT 36240
|||||
Db 36181 GATTCGAATATTCCTGATTAACGAGGCGCGCGCTTACGATTAATTCGATTAACAT 36240
QY 36241 TTAAGTGAACAGATATTTTCCAAACCCAAACGCTGCAATAGACGCTTAAATAA 36300
|||||
Db 36241 TTAAGTGAACAGATATTTTCCAAACCCAAACGCTGCAATAGACGCTTAAATAA 36300
QY 36301 AGGTGTGATAGCTTTAGTTTAAATTAAGTAAACATTAATAGATTTGCGCGCG 36360
|||||
Db 36301 AGGTGTGATAGCTTTAGTTTAAATTAAGTAAACATTAATAGATTTGCGCGCG 36360
QY 36361 TGCATTAATGTCAAGGCTTAAACGCGGTAATGCGGCTGCTGCTATTTGTGCGCGCG 36420
|||||
Db 36361 TGCATTAATGTCAAGGCTTAAACGCGGTAATGCGGCTGCTGCTATTTGTGCGCGCG 36420
QY 36421 GAACCCATGCGCAAAATAATGTCTGCGAGTAAACAGTCCGACATTTGACCTGCTG 36480
|||||
Db 36421 GAACCCATGCGCAAAATAATGTCTGCGAGTAAACAGTCCGACATTTGACCTGCTG 36480
QY 36481 GTGCGTGGCGGTTGCTTGAAGATGATTCGAAGTTTATTAATCCGCGGAGCGGCTA 36540
|||||
Db 36481 GTGCGTGGCGGTTGCTTGAAGATGATTCGAAGTTTATTAATCCGCGGAGCGGCTA 36540
QY 36541 CATTAAGTGGGCGGCTTGGATGATTCGTTGCTGCTGCTGCTGCTGCTGCTGCTGCT 36600
|||||
Db 36541 CATTAAGTGGGCGGCTTGGATGATTCGTTGCTGCTGCTGCTGCTGCTGCTGCTGCT 36600
QY 36601 GTTATCTGTTTGTATTTGTAAGATTAACGCGGTGGGCTGTGAAGGCTGCGCGGAGCA 36660
|||||
Db 36601 GTTATCTGTTTGTATTTGTAAGATTAACGCGGTGGGCTGTGAAGGCTGCGCGGAGCA 36660
QY 36661 AATGCGCTGCGAGTGAAGAAAGAGAGTTACTGCAATCACTAATTTTGAATTCGCTA 36720
|||||
Db 36661 AATGCGCTGCGAGTGAAGAAAGAGAGTTACTGCAATCACTAATTTTGAATTCGCTA 36720
QY 36721 ATTGCTGTGCTCCCAAGTCAAGTCAAGTCAATTAATGAGGCTGTGCAACATGATACGCT 36780
|||||
Db 36721 ATTGCTGTGCTCCCAAGTCAAGTCAAGTCAATTAATGAGGCTGTGCAACATGATACGCT 36780
QY 36781 CTCTGCGCTTGTGCTGCTCCACGACGACAGCAAGCAGCTGTTAAGCGGATGAGGATGAC 36840
|||||
Db 36781 CTCTGCGCTTGTGCTGCTCCACGACGACAGCAAGCAGCTGTTAAGCGGATGAGGATGAC 36840
QY 36841 ACCATTAATTCGACGATTTGATTAATTCGAGACGTTTGGGCGGTACAAATGCAATGTTT 36900
|||||
Db 36841 ACCATTAATTCGACGATTTGATTAATTCGAGACGTTTGGGCGGTACAAATGCAATGTTT 36900
QY 36901 GAATTAATGCTGCTGAATTTTAAACAACAGGGAAGGCTGCGCGGCTGCGGAGT 36960
|||||
Db 36901 GAATTAATGCTGCTGAATTTTAAACAACAGGGAAGGCTGCGCGGCTGCGGAGT 36960
QY 36961 CCGACCATTTGCGGCAAGTCCGACGACGACGACGACGACGACGACGACGACGACGACG 37020
|||||
Db 36961 CCGACCATTTGCGGCAAGTCCGACGACGACGACGACGACGACGACGACGACGACGACG 37020
QY 37021 AGCTGACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 37080
|||||
Db 37021 AGCTGACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 37080
QY 37081 CTTTGTGATGTTTCAAGAACCGGAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 37140
|||||
Db 37081 CTTTGTGATGTTTCAAGAACCGGAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 37140
QY 37141 TCTCAGTGAAGTCCCAACGCTTAATTAAGTGTGCAATTAACCTGCGGTTTAAAGTTGA 37200
|||||

D	37141	TTCTCCAGTGAAGTCCCAAAACGCTAATAGTGTGTGCAATTTACCTGCGGTTTAAAGTTTA	37200	D	38221	CGAAAACATGCGCTTAGAGCCGAGCGCTTTGCCCTTGCCGCCCAAGAACCTGCTTTAGG	38280
Q	37201	AAACGGGTGACGGTCTGATGATGAAAGACATAAAATTTGGGCTGCGTCTTAACCTGTC	37260	Q	38281	ATACAGCCCTGTGCGACGAATGCGACACAGTGTTCGCCACAGACATGACATTTGCGACGG	38340
D	37201	AAACGGGTGACGGTCTGATGATGAAAGACATAAAATTTGGGCTGCGTCTTAACCTGTC	37260	D	38281	ATACAGCCCTGTGCGACGAATGCGACACAGTGTTCGCCACAGACATGACATTTGCGACGG	38340
Q	37261	TAAACGGTATTTTCTTACTTGCAGACGATATCTTTGGAATGAGTTCATTTTATATTC	37320	Q	38341	GAATATTTGGTACCTTGGGTTGGAACGTTAGATAGTACGTTGACTTTGGCGTCACAAAC	38400
D	37261	TAAACGGTATTTTCTTACTTGCAGACGATATCTTTGGAATGAGTTCATTTTATATTC	37320	D	38341	GAATATTTGGTACCTTGGGTTGGAACGTTAGATAGTACGTTGACTTTGGCGTCACAAAC	38400
Q	37321	CAGAAATAGCGCATTTGCTGTGTTCTTGTGATGATGATGATGATGATGATGATGATGATG	37380	Q	38401	TACCTTTGACGGTGTGTTTGGCGGATGCTTTTGTATTTTACCTGATGATTTAGATC	38460
D	37321	CAGAAATAGCGCATTTGCTGTGTTCTTGTGATGATGATGATGATGATGATGATGATGATG	37380	D	38401	TACCTTTGACGGTGTGTTTGGCGGATGCTTTTGTATTTTACCTGATGATTTAGATC	38460
Q	37381	CGTACCAAGCGCGGCGCGGCTTCAGGCTCCAGATCCAAACGCAAAACGCAACACA	37440	Q	38461	AAGCATTTGATTTACTATGTTTGGTGTATGATGATGATGATGATGATGATGATGATGATG	38520
D	37381	CGTACCAAGCGCGGCGCGGCTTCAGGCTCCAGATCCAAACGCAAAACGCAACACA	37440	D	38461	AAGCATTTGATTTACTATGTTTGGTGTATGATGATGATGATGATGATGATGATGATGATG	38520
Q	37441	TTCCACCAAAACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	37500	Q	38521	CTGAATTTGTTTCTTCTTGGAGAGTTTTAAAGTACCGGATTTGATGATGATGATGATG	38580
D	37441	TTCCACCAAAACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	37500	D	38521	CTGAATTTGTTTCTTCTTGGAGAGTTTTAAAGTACCGGATTTGATGATGATGATGATG	38580
Q	37501	CTCCAGCGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	37560	Q	38581	AATATTTACCGTTTGGACGCGATGCGATGCGATGCGATGCGATGCGATGCGATGCGATG	38640
D	37501	CTCCAGCGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	37560	D	38581	AATATTTACCGTTTGGACGCGATGCGATGCGATGCGATGCGATGCGATGCGATGCGATG	38640
Q	37561	TATTTGGTTCATTTATCCGAAAGTTTAAAGTAAAGGCGCTACCGTATATTTAGAAAT	37620	Q	38641	CAAAATTTAAATTTTAAAGTAAATTCAGATGATGATGATGATGATGATGATGATGATG	38700
D	37561	TATTTGGTTCATTTATCCGAAAGTTTAAAGTAAAGGCGCTACCGTATATTTAGAAAT	37620	D	38641	CAAAATTTAAATTTTAAAGTAAATTCAGATGATGATGATGATGATGATGATGATGATG	38700
Q	37621	TGTCGAGTGGCGCTTAAACGAGAAAGTGTGATGATGATGATGATGATGATGATGATGATG	37680	Q	38701	TAGCGTGAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	38760
D	37621	TGTCGAGTGGCGCTTAAACGAGAAAGTGTGATGATGATGATGATGATGATGATGATGATG	37680	D	38701	TAGCGTGAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	38760
Q	37681	AGGGAATTAAGTGTGTCAGAAACGCTCTGCGCGCGCTGTAATGATGATGATGATGATG	37740	Q	38761	CAGATTTCCCGGAGTGTGCGGTAAGGCGCAAAAGCATTCCTGCAATTTCCATTTTGG	38820
D	37681	AGGGAATTAAGTGTGTCAGAAACGCTCTGCGCGCGCTGTAATGATGATGATGATGATG	37740	D	38761	CAGATTTCCCGGAGTGTGCGGTAAGGCGCAAAAGCATTCCTGCAATTTCCATTTTGG	38820
Q	37741	AAAGCCGTGAGAGTCTAACGATGATGATGATGATGATGATGATGATGATGATGATGATG	37800	Q	38821	AAGGTAAAGCAGAGAGATTCGAAACATGCTTTGATTAATTTACGCAATATTAATG	38880
D	37741	AAAGCCGTGAGAGTCTAACGATGATGATGATGATGATGATGATGATGATGATGATGATG	37800	D	38821	AAGGTAAAGCAGAGAGATTCGAAACATGCTTTGATTAATTTACGCAATATTAATG	38880
Q	37801	CACCGGTAAAGACCTGAGAGTTCCTATGACGAACTAAAGTGCACATGATGATGATGATG	37860	Q	38881	CGAAGATGACGACGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG	38940
D	37801	CACCGGTAAAGACCTGAGAGTTCCTATGACGAACTAAAGTGCACATGATGATGATGATG	37860	D	38881	CGAAGATGACGACGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG	38940
Q	37861	TATGTTAACTGTTAATGAGCCCGCTGACAGGTTGCGAGTGAACACATCAGCAGT	37920	Q	38941	TTGCTAGGTGAAGACGTTGGGTAAAGCATGATGATGATGATGATGATGATGATGATGATG	39000
D	37861	TATGTTAACTGTTAATGAGCCCGCTGACAGGTTGCGAGTGAACACATCAGCAGT	37920	D	38941	TTGCTAGGTGAAGACGTTGGGTAAAGCATGATGATGATGATGATGATGATGATGATGATG	39000
Q	37921	GAATGAGGTTCTTCTTACAGGAGATTTTTCATTAACAAGTTATAGTACGCTGAGGAT	37980	Q	39001	GATAGCATCATCATTTATTAACCCCGTCCGCTACTGCTTACCGGCTTTGCGCAAGAT	39060
D	37921	GAATGAGGTTCTTCTTACAGGAGATTTTTCATTAACAAGTTATAGTACGCTGAGGAT	37980	D	39001	GATAGCATCATCATTTATTAACCCCGTCCGCTACTGCTTACCGGCTTTGCGCAAGAT	39060
Q	37981	GTCGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	38040	Q	39061	ACGACCTTGGGCGGTATTAAGAGGTATAGTCTTCCCAATTCAGACGCGGAGCGC	39120
D	37981	GTCGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	38040	D	39061	ACGACCTTGGGCGGTATTAAGAGGTATAGTCTTCCCAATTCAGACGCGGAGCGC	39120
Q	38041	CATATTTGATTTGAAACTGAGATTTGAACTGTGTAACACTATGCTTAACCTGATC	38100	Q	39121	ACGACGCGGTAAAGGTGCTCTGTTTGCATGACCCCTGTCGAAGGCTCTTACGAGAC	39180
D	38041	CATATTTGATTTGAAACTGAGATTTGAACTGTGTAACACTATGCTTAACCTGATC	38100	D	39121	ACGACGCGGTAAAGGTGCTCTGTTTGCATGACCCCTGTCGAAGGCTCTTACGAGAC	39180
Q	38101	GAACATGTCGAGAGGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	38160	Q	39181	GTTTTCAGAGATCTCATTTATTTGGTGGCGAGGCAACAAATTTGCCAGTTGAGTTTAA	39240
D	38101	GAACATGTCGAGAGGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	38160	D	39181	GTTTTCAGAGATCTCATTTATTTGGTGGCGAGGCAACAAATTTGCCAGTTGAGTTTAA	39240
Q	38161	GTTTTCAGAGATCTCATTTATTTGGTGGCGAGGCAACAAATTTGCCAGTTGAGTTTAA	38220	Q	39241	ATCGGAATTTGGCGGTGACGCGGCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	39300
D	38161	GTTTTCAGAGATCTCATTTATTTGGTGGCGAGGCAACAAATTTGCCAGTTGAGTTTAA	38220	D	39241	ATCGGAATTTGGCGGTGACGCGGCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	39300
Q	38221	CGAAACATGCGCTTAGAGCGGAGCGTTTCCCTGCGCCGAAACCTGCTGTTAGG	38280	Q	39301	AACAGGCGCTGCAACAGCATTAATGAGGCGGCTCTGAGAGTACGACCTTTCCATTTAT	39360
D	38221	CGAAACATGCGCTTAGAGCGGAGCGTTTCCCTGCGCCGAAACCTGCTGTTAGG	38280	D	39301	AACAGGCGCTGCAACAGCATTAATGAGGCGGCTCTGAGAGTACGACCTTTCCATTTAT	39360

QY	39361	GGCCAGGAGGCCAATCTGCTTCGTCAATAATGAAAGAGTCCGGAGCGACGACTTTTAA	39420
Dd	39361	GGCCAGGAGGCCAATCTGCTTCGTCAATAATGAAAGAGTCCGGAGCGACGACTTTTAA	39420
QY	39421	AACTTTTCAACTGCTGTGGGAAAGACGCCAGGAGGAGGATTCATTTGAGGGTCT	39480
Dd	39421	AACTTTTCAACTGCTGTGGGAAAGACGCCAGGAGGAGGATTCATTTGAGGGTCT	39480
QY	39481	TTTGGGGCGTGTATACCAACAGTAATTCAGTTTGTGAATTTCTTGGAACGTCGCTAGCGGT	39540
Dd	39481	TTTGGGGCGTGTATACCAACAGTAATTCAGTTTGTGAATTTCTTGGAACGTCGCTAGCGGT	39540
QY	39541	TGGGTGGGTAAACACGAGTTTAAAGACCTCAACGAATGACGGATGGAAATTCAGTT	39600
Dd	39541	TGGGTGGGTAAACACGAGTTTAAAGACCTCAACGAATGACGGATGGAAATTCAGTT	39600
QY	39601	TAAAGTATCTGTACCCAGCATCTGCTATGGGGAGCGGACGCGCCACAAAACAAAACA	39660
Dd	39601	TAAAGTATCTGTACCCAGCATCTGCTATGGGGAGCGGACGCGCCACAAAACAAAACA	39660
QY	39661	ATACATATTATCATAAGAGCGCTGCATATTAAGCATCATTTGGTGGCGAGATAGACTCTCGAC	39720
Dd	39661	ATACATATTATCATAAGAGCGCTGCATATTAAGCATCATTTGGTGGCGAGATAGACTCTCGAC	39720
QY	39721	TGATGACATTCGAGCTGCTATTCATTACAGAGAAAACCCACTTCGATTACACGAATAGCC	39780
Dd	39721	TGATGACATTCGAGCTGCTATTCATTACAGAGAAAACCCACTTCGATTACACGAATAGCC	39780
QY	39781	CGGGGCGGTAAAGACGATTACCGCCCTCTCCAGTTTGGCGTGGAGCGGCTGGAGAGGG	39840
Dd	39781	CGGGGCGGTAAAGACGATTACCGCCCTCTCCAGTTTGGCGTGGAGCGGCTGGAGAGGG	39840
QY	39841	CCTGTAGATACCGCTATTGTAATGTTAAGCTTAGTCCGCCCGCGAGTGTATTCTAAA	39900
Dd	39841	CCTGTAGATACCGCTATTGTAATGTTAAGCTTAGTCCGCCCGCGAGTGTATTCTAAA	39900
QY	39901	AACACTATTCAGACCCGGGTCTACACCGCAAGGGGTCTTAAAGAGGCTGTTAACTCAGACAT	39960
Dd	39901	AACACTATTCAGACCCGGGTCTACACCGCAAGGGGTCTTAAAGAGGCTGTTAACTCAGACAT	39960
QY	39961	GGTGTCCATGTTCAAAAGCTACTTATTGGTAACTCGTTT	40000
Dd	39961	GGTGTCCATGTTCAAAAGCTACTTATTGGTAACTCGTTT	40000
RESULT 2			
LOCUS	AF210726	130733 bp DNA linear VRL 27-MAR-2000	
DEFINITION	Mecaca mulatta rhadinovirus 26-95 long unique region L-DNA, complete sequence.		
ACCESSION	AF210726		
VERSION	AF210726.1		
KEYWORDS	AF210726.1 GI:7329990		
SOURCE			
ORGANISM	Mecaca mulatta rhadinovirus 26-95		
REFERENCE	Mecaca mulatta rhadinovirus 26-95		
AUTHORS	Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Gammaherpesvirinae; Rhadinovirus.		
TITLE	1 (bases 1 to 130733)		
JOURNAL	Alexander, L., Denekamp, L., Knapp, A., Auerbach, M.R., Damania, B. and Desrosiers, R.C.		
MEDLINE	The primary sequence of rhesus monkey rhadinovirus isolate 26-95: sequence similarities to Kaposi's sarcoma-associated herpesvirus and rhesus monkey rhadinovirus isolate 17577		
PUBMED	J. Virol. 74 (7), 3388-3398 (2000)		
REFERENCE	2 (bases 1 to 130733)		
AUTHORS	Alexander, L., Denekamp, L.M., Knapp, A., Auerbach, M., Czajak, S., Damania, B. and Desrosiers, R.C.		
TITLE	Direct Submission		
JOURNAL	Submitted (02-DEC-1999) Microbiology, New England Regional Primate Research Center, One Pinehill Dr, Southborough, MA 01772, USA		

FEATURES

source

location/Qualifiers

1..130733

/organism="Macaca mulatta rhadinovirus 26-95"

/mol_type="genomic DNA"

/isolate="Macaca mulatta rhadinovirus isolate 26-95"

/db_xref="taxon:119193"

513..1784

/gene="R1"

513..1784

/gene="R1"

/codon_start=1

/product="ORF1"

/protein_id="AAFS9980.1"

/db_xref="GI:7329991"

/translation="MFVYLFLMLQPVSVLLPAKLTSTVFQCPHPHGDYLLTCRST
STARDDQSTQMFNNMTLMRSGNSYGRGLVSTYPNATYSIDRAACQTKTTTSSNNIDPFRS
SSRLTIDERSGSYGTYAANTRVLRCSGDNVLRNVPFLNGTAVNGTTRRHIFPV
LTEKGTGYFCSAFIEGNEKFSQTIINVFSEPFKPNIDPNSEHFKSQIOQTASV
QHPENYVSVFVPVPSIVLTGLIASLIMCLFLTRCNSESSNSHSAQSTYSIOPHS
NQSNTNECSRHTHYRRNAHQBESIEELPNQTSSETDSCQVLLEKRVATDQGEQNTI
NEWEQYDIDVVENIETQTSYEDNVEHMDYSQTIINPNNTYSGLIEEDVEFYNELSN
QYHGLIENLNDHEYNLNLNMIEOYDML"

complement(1852..2418)

/gene="ORF02"

complement(1852..2418)

/gene="ORF02"

/codon_start=1

/product="DHF"

/protein_id="AAFS9981.1"

/db_xref="GI:7329992"

/translation="MDIAYNCIYAVDEQLGKNGTTPPYRLNEMMYPOKMTSPV
VGEINVIWGRKTWFSIPEKRRPLVNNITILSELHPHGAHFLARTLDDAFNFR
QYKRLQELNTVWVIGKSVYESVLTNKCPLKLYTRIMSEFDCDVFEPSTNTEYML
SELGKEDNFEENWIGKFKQYEXENK"

2595..3782

/gene="ORF04"

2595..3782

/gene="ORF04"

/codon_start=1

/product="complement binding protein"

/protein_id="AAFS9982.1"

/db_xref="GI:7329993"

/translation="MFWPTLFCICVILVDSKDGNYVCLAPPRDRFVYKRNQNE
NVAIGRVELICRPGEFKIQAANYVECLSGWTTTPAECRRKRCSPEDILGEVIT
TDSNARKFSGSNITTKCNTGYLLGAIVRCLKLYBSNLVDMQPAATCBIECKKQD
DIEGNKAFVQEFNYLEITFTFCNKFSLIGTTCMTGNNWSPVPCQITCSA
PNIDHGTLLVGSRSRYHGOSVITGCGDHLKHKCTEYSILANPFLPCVINKT
DPPSEYVSPGRTQEQEMPTPEPNKSHSETTTTETPKTQVKESETPKPKNPETHK
TTPBAGISKQTTTNRPSKAPSONPLAPMSKMRHVLLVLFASVSLFLVLAALVC
FLK"

4213..7611

/gene="ORF06"

4213..7611

/gene="ORF06"

/codon_start=1

/product="sDBP"

/protein_id="AAFS9983.1"

/db_xref="GI:7329994"

/translation="MASKGNAGPRLDNGSRAPICAGVYVASKDPFPAASLTG
NRSGSGVSESLPIYLGLTVEHERPLTYKAKYKVDITTLVAKVTCFIREYVFNHNSL
FRFVFGDTGLNELCEEARALFGYTOLEPSPHSIMPLRCPQLPDDDEHFLADVATE
GFERLMRGLPVPVFOQVOIAGROAFVPLYDEDLFAPHGRMRFRFHKVSAVL
YDSLEFISAOALRLKDYTAIVHATEKOFMODHYIAIYQAKFSTLLPTTQSSHM
IYQSVVLELALSYGCMFLGPCDACLNLDSMIPDGCSPPEARVALLRSGSEAV
HVAGQIPAANSVLYLTKVQQAQPGCKGVNVNNSPFLQGLSFLNATIKENSGEF
KQVSNALDSSFTPIYHAYAAFSPLKLKCLTYMOFLDHHSSITQATNMHVGFT
AANSEKOTLCHGNTPATCLNTLFYRLKDRPVAYTPQRPDPYVVTGAGFNDLELIG
NFASFCRREDGNDPDEHPKRYTYWOLQOTYETKLSAIGTEDHNNHNLITNOSLFR
VFGIDISIVDEGWAKEVNSAKNNFNREHKSVINHLIQCQNVYMOAPCAVELNLY
KSLIMLITODICLPLCYMTYEQDNPAMGILPSEMLKMHQOTLWPNKKAACIDRGVLGGE
LKIVHMRCDPFDPDGASNGCLAMPQVRIARIMMYVPKSITIKIRNITSENTPAGE
AVSGGEFYPKTGTDTTYVACPYKFLSLRLALRPDTKTALVLMKIRISQNTKTPVLK
DVDPDELAELVSYKINSIAFEEETNVLVDVPSLMSYARKLNGALIRACGQIQPFAV

THCLTPVLOTIDAEEXPHVLSAATPAVYLAIEIRGRTALTIVOTAROPVATGRL
RPTVPMYVANKITGVANGNNWPHCGMLGTFAGCVDRNIMPSSPRTKTSVSMMLK
RHVMPTIDRLIKRAGQITSTFEASVRSVQALLIEDKNPLKSVLLEILRLHG
KGCODLSEEDVQYLLIDYCMJTEVLTLDNIAGSGPWTIEDGALIEDRODADDIQ
FVSDDIATASCPPEEQPLTPPSAGALLACKRKRIINALLSLDL"
7636..9696
/gene="orf07"
7636..9696
/gene="orf07"
/codon_start=1
/product="transport protein"
/protein_id="AAFS9984.1"
/db_xref="GI:7329985"
/translation="MARELAALAOALSALAVDLSLVTFADPPRSIDGARILKTQLEN
LNRLPLELKEQSVETSLSEVHEHLAKNIEKLGELSLKQRYSSRHEFTLHLR
PECHYHSTVEFOEGGLIDVNNCLINDVELCKRSLSVYCIGANGCLGKLVLE
LSTRLGISPIPHDLVYTVPCVOCLEIELVNOGSLIADLRCHDCLCKVRE
PIHGFETELSQGLKVTKRSDATOGHVRSSDOLRESSLAIODHNIKFRVASIME
LSNLIYVNAQOTGLOGTENEGSOMARLLTHEADMEHRLALITPKLSATHFYCCFRD
PIESICGGI.FNSIDDTINLSRDCSTTFQOANTYVMKQNELFRILMSILROGSA
GSOXPATPSERTTTVAATIASVYIKDAQTRKQYMKKVARDEKRLTECLOQGAUL
ANLCKRWGVAVGEASELVNHFLLRRFVALPWEARCRSDILFENSKYIKNSLVS
QRLSREHVEIITLOFGLITGPLRQSDLPFPANVYLAQCFEAGMLPHHKMLVSM
IMPQIOPKMDIOTFNRFYQLPEGDINAQKSAKCFIRELVLSVALINRTMEKTRIF
SLAREKLSINLDVKLGSLVLYEQDAPLVLSQNTGWIIFKDIYALLXHLHQLSDG
HDN"

gene
9683..12172
/gene="orf08"
9683..12172
/gene="orf08"
/codon_start=1
/product="orf08"
/protein_id="AAFS9985.1"
/db_xref="GI:7329986"
/translation="MMIINTRLRLAMVYIIAIGTAVGENTTPKGAITTAKTPEP
STPPENPRAAFKFRVCSASATGELFEFNLEKCPGEDTKDQEGILMTPTGP
PHFKRYRKVATSVTVYKRGTEATVAGOEYIRPPOYEIHMPTDYCCFSMRN
VNGIVMYDRDPTNOTFLOPEGLNDINOYRFOYPLVYTPGMPGIRVRYTVC
EIVDMTARSAPYSYFVALGDTVSESPCHNDSTCSVAKTENGSLVRLNTTYVD
FATRKPTERRVADSGEYTVKMAEDPSAVCALILMKTFHTPAIOTTHEASHYFAN
DVATFTSLSEVANTGTYSCLDEVIQKLNQTIKLSLHTEVNSADQYKKEGFL
LMOPLPLSLVDEMRLNGTTPAPATSTSVRSVNTNQANDNLNAPOLQFAY
DKLRASINKVLEELSRAMCQEOYRDTYMWELSKINPTSWATIGRPAKVGVAL
SYTDCVAVDOASVSIKSLRSTPGMCYSRPVTPFPFNTLILFKGOLGPRNLIITLD
NOVEACKETCEHFIAISNVTYKDYCPFKKITSFSLTGFIATLNSLTENIDRV
IELYSRAEKKLSGVPTDIEMREYNTYTORLGLNEDNDITDLNLRSTENIDRV
ADLGDGRTVVNAVSSVITLFGSIVSGFINFKSPFGMIMLIVIAVAVILVFLMR
TNAIAGAPTRMTPDIDMKQPSGKVDQEDQIKNIAGMHQLOOEERRRDEQSRAPS
LFRRAADGKRRRGYKPLENEAOEYEMSK"

gene
12290..15334
/gene="orf09"
12290..15334
/gene="orf09"
/codon_start=1
/product="polymerase"
/protein_id="AAFS9986.1"
/db_xref="GI:7329987"
/translation="KDFENPYLGPRGPRPHSHRGTDAPAPAGAVOPPDVCRLLPA
CLTPGAGMIPVTPPEPTFENGARGVLLANERSMTARBRKVAADPODOSTIF
HAYDVETTYAADRCALVPSRFOTDIPSGTVLLEKNSGVCVAVPFOOVYVA
KYPAGINTHILQOALKNTAGRAAGCFSTRVYKRLIKTYDDAEHVTEITLSSGML
STLSDBLVACGGEVESNDVARRVLDGCTFTGYSARATPRIAADARTRALEFD
CSWEDLSVQADSDDPPRIVAFDIECTEAGPCYTRGDVNTQISCVFYTREAP
NPNLIFSVGTCDIPDIDVLEPSEYDMLVSEFAMRINQEFKILGIVIPIMYOYCR
ITRASOVNMLRNEPYKIKTGSIFEVHEHGGGSGFMARSVKIKIGVIPIMYOYCR
EKLSIDYKIDTVAROCLEKKEDEVYKDIPLFRSGPGRAKVGSGYCVMSDVLVNDL
LKMFMIHVEISLAKLQIARVRVLTDGOLRVFQLLEAARENNIIPVPEEGG
YOGATYINPIRSGYDEPVYVDPASISYIIOAHNICYTHIHGRDLHLPNITPDDY
EFTVLSGGVHFVKKHRESLLGLTLVLEKRRALRRLTALACDDPSLTIIDKQOLA
IKVTCNAVGTGTVASGLPCINIAETVTLRGRTMLEKMSYVEALITPDLTRGLRE
VTARHGARFVYGDTSFLIACDGSASAVAFCDMLAARTADLEPPRIKLEAKT
FCLILLTKRKYIGVLNDKMKMGVDLIRTKAKFVORCAHLLIDVYHDEEVAAA
RLCKRPPHAYVEEGIPAGFIKIVEVLANSYDLRNSVPIQLITFSTLSRVCYDK

gene
12290..15334
/gene="orf09"
12290..15334
/gene="orf09"
/codon_start=1
/product="polymerase"
/protein_id="AAFS9986.1"
/db_xref="GI:7329987"
/translation="KDFENPYLGPRGPRPHSHRGTDAPAPAGAVOPPDVCRLLPA
CLTPGAGMIPVTPPEPTFENGARGVLLANERSMTARBRKVAADPODOSTIF
HAYDVETTYAADRCALVPSRFOTDIPSGTVLLEKNSGVCVAVPFOOVYVA
KYPAGINTHILQOALKNTAGRAAGCFSTRVYKRLIKTYDDAEHVTEITLSSGML
STLSDBLVACGGEVESNDVARRVLDGCTFTGYSARATPRIAADARTRALEFD
CSWEDLSVQADSDDPPRIVAFDIECTEAGPCYTRGDVNTQISCVFYTREAP
NPNLIFSVGTCDIPDIDVLEPSEYDMLVSEFAMRINQEFKILGIVIPIMYOYCR
ITRASOVNMLRNEPYKIKTGSIFEVHEHGGGSGFMARSVKIKIGVIPIMYOYCR
EKLSIDYKIDTVAROCLEKKEDEVYKDIPLFRSGPGRAKVGSGYCVMSDVLVNDL
LKMFMIHVEISLAKLQIARVRVLTDGOLRVFQLLEAARENNIIPVPEEGG
YOGATYINPIRSGYDEPVYVDPASISYIIOAHNICYTHIHGRDLHLPNITPDDY
EFTVLSGGVHFVKKHRESLLGLTLVLEKRRALRRLTALACDDPSLTIIDKQOLA
IKVTCNAVGTGTVASGLPCINIAETVTLRGRTMLEKMSYVEALITPDLTRGLRE
VTARHGARFVYGDTSFLIACDGSASAVAFCDMLAARTADLEPPRIKLEAKT
FCLILLTKRKYIGVLNDKMKMGVDLIRTKAKFVORCAHLLIDVYHDEEVAAA
RLCKRPPHAYVEEGIPAGFIKIVEVLANSYDLRNSVPIQLITFSTLSRVCYDK

TTNLPPLAVOKLASRCEELPQVHDIRLPYFVDAPSGLKDLAEHPDYVROHOIPVAV
DLFYDKLVHGAANLLOCLFGNNADTVAIILNPLNPKLS"
15429..16679
/gene="orf10"
15429..16679
/gene="orf10"
/codon_start=1
/product="orf10"
/protein_id="AAFS9987.1"
/db_xref="GI:7329988"
/translation="MLVNTLSVYIGMEVTFHRRGFSVNLTRLOTFKGGHGYARVL
PESIDOLHOPAPAGLYTRKELPRESDCYALAIPLDSGDAARAVARPEVDSRSP
LTVVNSGHTTRFCLFLKLPIDLERAVTVFENGAGSESTPRKCTESLPQGP
LRVNSQSQTSFSPSEVAFYFTANSVACLILRLQVRFPSDDAARARISPKYVTSN
SGNVKASVHTLSPSKCTKQMEIITYAPDPMAEIYLGSGVFLPTHTGGRYLVYA
DARKTQPGSSAARVOLIQOQAAARGDLAFVTGVAPELIPVYIPALLSCCTHL
RLNPNTPTTTRDTLVAAACCPVYRLSSADAPRDVLAASPDGALSNATPIYVG
FPCVSAECSVSI.RDNGVHERNMH"

gene
16688..17917
/gene="orf11"
16688..17917
/gene="orf11"
/codon_start=1
/product="orf11"
/protein_id="AAFS9988.1"
/db_xref="GI:7329989"
/translation="MGTVPFRFEGEMQTSVLDNGCPRRYSLSLWMAATIHQVLTLYNR
SELCTVRSFCLPACPSIGRLVGRKRFPGFAFATLGRTRTFVFAFGIRNDPLDI
PAVERADRELVLVHAQPTTRVSRGLKFAVIAIVVRRPVGFLHFPORVIALTD

Query Match	26.94;	Score 10772;	DB 1;	Length 130733;
Best Local Similarity	99.48;	Pred. No. 0;		
Matches 15792;	Conservative	0;	Mismatches 98;	Indels 1;
QY	5489	CACAAATCCACCAATAGACACCCCAATGAGTAATGAAAGCATGTCGTATGTC	5548	
DB	3658	CACAAATCCACCAATAGACACCCCAATGAGTAATGAAAGCATGTCGTATGTC	3717	
QY	5549	TTTTTGCAGTGTGCGGCTCTTGTATGCTACTGTCGCTTATGTTGTTCTAA	5608	
DB	3718	TTTTTGCAGTGTGCGGCTCTTGTATGCTACTGTCGCTTATGTTGTTCTAA	3777	
QY	5609	AATAAGCTTTTGCTTCAGCAGGTGCGGCAACTGCGACGCAATTAACCAATCT	5668	
DB	3778	AATAAGCTTTTGCTTCAGCAGGTGCGGCAACTGCGACGCAATTAACCAATCT	3837	
QY	5669	GCCAAACCGCGTGTATCCGGAATTAAGTTACATTATTCAGGTTGCCAATAAGGTGG	5728	
DB	3838	GCCAAACCGCGTGTATCCGGAATTAAGTTACATTATTCAGGTTGCCAATAAGGTGG	3897	
QY	5729	TTTAAATATTTTATGTTGTTCTATGTTTATGTTACCGCGTTATAGTATCGCGCC	5788	
DB	3898	TTTAAATATTTTATGTTGTTCTATGTTTATGTTTACCGCGTTATAGTATCGCGCC	3956	
QY	5789	ACCTTGCGCTACATATATAGCAGATACCTTCACGTTATACCTTACCGACATATGA	5848	
DB	3957	ACCTTGCGCTACATATATAGCAGATACCTTCACGTTATACCTTACCGACATATGA	4016	
QY	5849	CITCATAGCGCTTACGTCACGTGCGCTGCGATTTGGCGGGCTAAATAACACAAGG	5908	
DB	4017	CITCATAGCGCTTACGTCACGTGCGCTGCGATTTGGCGGGCTAAATAACACAAGG	4076	
QY	5909	GGTACATTAATCATTCAGGCGGACACATTAAGACAGGTTTATAAACTATATCGGATGC	5968	
DB	4077	GGTACATTAATCATTCAGGCGGACACATTAAGACAGGTTTATAAACTATATCGGATGC	4136	
QY	5969	GCCAAATCATCTGTCGTAGGACACATTAAGAAAAACATTTTAACGTTGTTAGGCA	6028	
DB	4137	GCCAAATCATCTGTCGTAGGACACATTAAGAAAAACATTTTAACGTTGTTAGGCA	4196	
QY	6029	ACTGGAATTAACATTAATGCTTCCAAAGGCAAGCGGACGACAAACCCCTGGAATTAATGA	6088	
DB	4197	ACTGGAATTAACATTAATGCTTCCAAAGGCAAGCGGACGACAAACCCCTGGAATTAATGA	4256	

OY	6089	GGGCTCTCGTGGCCCCGATAGGTGCGTGGGATGTACGTGTACGGCTGATTTCCGAAACAGACTT	6148
Db	4257	GGGGTCCCGTGGCCCCGATAGGTGCGTGGGATGTACGTGTACGGCTGATTTCCGAAACAGACTT	4316
OY	6149	TTCCTTTGGCGAGGCGTCCATACCTCCGGCAACAGACATCTGGATCTGGCGTTTCTCGCT	6208
Db	4317	TTCCTTTGGCGAGGCGTCCATACCTCCGGCAACAGACATCTGGATCTGGCGTTTCTCGCT	4376
OY	6209	ACCAATCCCTTTACGGACTTACAGTTTGAACACGATTTCCCTCTCAACCGTAAAGCCGCAT	6268
Db	4377	ACCAATCCCTTTACGGACTTACAGTTTGAACACGATTTCCCTCTCAACCGTAAAGCCGCAT	4436
OY	6269	CAAAAAGATTGACACACAGACGCTCCGCCGTTAAGTGAAGCTGCTTTCCACAGAGAGTTAT	6328
Db	4437	CAAAAAGATTGACACACAGACGCTCCGCCGTTAAGTGAAGCTGCTTTCCACAGAGAGTTAT	4496
OY	6329	TGTGTTTCCACATGCAGTTTATTTACAGCGCGTGTTTGACGCTACCGGTCTTAACGAACT	6388
Db	4497	TGTGTTTCCACATGCAGTTTATTTACAGCGCGTGTTTGACGCTACCGGTCTTAACGAACT	4556
OY	6389	ATGCGAGGAACCCAGGCGCTCTTTTGGGTCACCCAGTTTATTAACCCGGGTCACCTCA	6448
Db	4557	ATGCGAGGAACCCAGGCGCTCTTTTGGGTCACCCAGTTTATTAACCCGGGTCACCTCA	4616
OY	6449	CAGCATATGGAACCCCTCTGGAATCTCCGACGTTACCGGACAGAGATGATGTTTCTTGG	6508
Db	4617	CAGCATATGGAACCCCTCTGGAATCTCCGACGTTACCGGACAGAGATGATGTTTCTTGG	4676
OY	6509	CGTTGTTTGTGCGAAGGGGTTTAAGGAAAGCTGTGAGAGGGGCGTCTCGTTCCCGGGT	6568
Db	4677	CGTTGTTTGTGCGAAGGGGTTTAAGGAAAGCTGTGAGAGGGGCGTCTCGTTCCCGGGT	4736
OY	6569	GTTCCAGACCCAGAGGTGTCAGATTGGCCGAGCGACGCGCTTTAAAGTGCCGTGTGACGA	6628
Db	4737	GTTCCAGACCCAGAGGTGTCAGATTGGCCGAGCGACGCGCTTTAAAGTGCCGTGTGACGA	4796
OY	6629	CGAAGACTGTTTGTGACCTCAACGGTCATAGAATGCCAAGGTTTAAACATAAAGACGTTAG	6688
Db	4797	CGAAGACTGTTTGTGACCTCAACGGTCATAGAATGCCAAGGTTTAAACATAAAGACGTTAG	4856
OY	6689	CGCGTACCTTACGACACTCCCTCTTTACAGAGATGGCCAGGCGCTGTGAGACTCAAGAAGCT	6748
Db	4857	CGCGTACCTTACGACACTCCCTCTTTACAGAGATGGCCAGGCGCTGTGAGACTCAAGAAGCT	4916
OY	6749	GACGGCGGTCTATCCAGCGCACAGAAAGCAATTCATGCGAGGACCATTTACAAATTTGCCAA	6808
Db	4917	GACGGCGGTCTATCCAGCGCACAGAAAGCAATTCATGCGAGGACCATTTACAAATTTGCCAA	4976
OY	6809	GATAGTGCAGCAAAACAGTTTTCAAAGAGCGCTCCGAAAAAGACAGACGGGTGTGCCCA	6868
Db	4977	GATAGTGCAGCAAAACAGTTTTCAAAGAGCGCTCCGAAAAAGACAGACGGGTGTGCCCA	5036
OY	6869	CATATATTGTGACAGCGTCTGTCGCGACGACTGGCCCTTAGTTACGGCTGTATGTTTCTCGA	6928
Db	5037	CATATATTGTGACAGCGTCTGTCGCGACGACTGGCCCTTAGTTACGGCTGTATGTTTCTCGA	5096
OY	6929	GTTGTCGCCAGAGCGGTGCGAATTCGTAACACTGAGTACGCTGAGCCCATATTTTGTGTTGG	6988
Db	5097	GTTGTCGCCAGAGCGGTGCGAATTCGTAACACTGAGTACGCTGAGCCCATATTTTGTGTTGG	5156
OY	6989	TGACTCACCAGAGGCTTAGGTTTAAACGGTTTAAAGACGCTGTGCGGCCGCAACAGCCGCTTCA	7048
Db	5157	TGACTCACCAGAGGCTTAGGTTTAAACGGTTTAAAGACGCTGTGCGGCCGCAACAGCCGCTTCA	5216
OY	7049	CGTGGCGGGTCAACTGTTCCGTGCGCAATTCGGTCTGTACTTAACCTAAAGTGCAAGACGA	7108
Db	5217	CGTGGCGGGTCAACTGTTCCGTGCGCAATTCGGTCTGTACTTAACCTAAAGTGCAAGACGA	5276
OY	7109	AGCGCCCAAGGGGCAAAAAGGAGACGTAAACGTGTACACTCTCTTTTCTCCACAACAGG	7168
Db	5277	AGCGCCCAAGGGGCAAAAAGGAGACGTAAACGTGTACACTCTCTTTTCTCCACAACAGG	5336

[illegible]

|||||
Db 6417 CACCGCGGATCCGAGCGGATGCAAGTGGGGTGTAAACCGAGCGGAACCGAGGACAC 6476
QY 8309 TTACGTGTGGCGGACCGTACATGAGATTCTCACTCGCTCATGGCCGCTGTCC 8368
Db 6477 TTACGTGTGGCGGACCGTACATGAGATTCTCACTCGCTCATGGCCGCTGTCC 6536
QY 8369 CGACACCAAGACCGCGCGCTGTACTGTGTGGCAACAGATCTCCACACCAACAAACCC 8428
Db 6537 CGACACCAAGACCGCGCGCTGTACTGTGTGGCAACAGATCTCCACACCAACAAACCC 6596
QY 8429 AGTTCTGAAGAGCTCCCGGACGACGAGTGGGGAGCTGTGTGCTACGTAAAGACCA 8488
Db 6597 AGTTCTGAAGAGCTCCCGGACGACGAGTGGGGAGCTGTGTGCTACGTAAAGACCA 6656
QY 8489 CACCTTCGCTTCGAGGAAACGAAAGTGTGAGAGTGTTCGGAATTCACCTATCTGT 8548
Db 6657 CACCTTCGCTTCGAGGAAACGAAAGTGTGAGAGTGTTCGGAATTCACCTATCTGT 6716
QY 8549 CGGAGAGATCAAACTGAACGCGGGCATTTCTAAGGCATGTGGCCAGATTCTAGTTTACG 8608
Db 6717 CGGAGAGATCAAACTGAACGCGGGCATTTCTAAGGCATGTGGCCAGATTCTAGTTTACG 6776
QY 8609 CACGAGCTGCATGCTCAGCGCGGTGTACAGAGATGATCGGAGAAATACCCCA 8668
Db 6777 CACGAGCTGCATGCTCAGCGCGGTGTACAGAGATGATCGGAGAAATACCCCA 6836
QY 8669 CGTGTGGGCTCCGCGGCAATCGCACACCGGTGTACCTGTGAGAAATACGCGCCG 8728
Db 6837 CGTGTGGGCTCCGCGGCAATCGCACACCGGTGTACCTGTGAGAAATACGCGCCG 6896
QY 8729 CACCGGCTTCACCGTCCACAGACGCGCGGTGTACCGCCGACAGAGCGCTCGG 8788
Db 6897 CACCGGCTTCACCGTCCACAGACGCGCGGTGTACCGCCGACAGAGCGCGCTCGG 6956
QY 8789 TCCCGTATTAACCGTTCCCATGTGTACCAAAATACAGGGGTCAAGGGAAACAA 8848
Db 6957 TCCCGTATTAACCGTTCCCATGTGTACTCAAAATACAGGGGTCAAGGGAAACAA 7016
QY 8849 CGTTTTCACTGCGGAAACCTGGGGTACTTCCGCGGGCGGGGTGAGACCGCAACTGTG 8908
Db 7017 CGTTTTCACTGCGGAAACCTGGGGTACTTCCGCGGGCGGGGTGAGACCGCAACTGTG 7076
QY 8909 GCGGAAAGCTCCCGCTTTAAGAAACGGGCGTACAGCGCATGTCTAAGAAAGACAGT 8968
Db 7077 GCGGAAAGCTCCCGCTTTAAGAAACGGGCGTACAGCGCATGTCTAAGAAAGACAGT 7136
QY 8969 CATGATGACCCCATTTATGACGCGCTAATTAAGCAGCGCGGACAGACATTCAGC 9028
Db 7137 CATGATGACCCCATTTATGACGCGCTAATTAAGCAGCGCGGACAGACATTCAGC 7196
QY 9029 GTTCGAGCGGAAAGCGTTAAAGAGCGTGCAGCGCTGTGAAGATPAAGACAACC 9088
Db 7197 GTTCGAGCGGAAAGCGTTAAAGAGCGTGCAGCGCTGTGAAGATPAAGACAACC 7256
QY 9089 TAACCATTAAGATGAGTATCTGTGAGCTTATAGACACCTGGGAAAGGCTGCCAGA 9148
Db 7257 TAACCATTAAGATGAGTATCTGTGAGCTTATAGACACCTGGGAAAGGCTGCCAGA 7316
QY 9149 CTTAAGCTCCGAGAGCTGCAATATTAATCTCGGTGCTATTTGATTTGACGAGAGT 9208
Db 7317 CTTAAGCTCCGAGAGCTGCAATATTAATCTCGGTGCTATTTGATTTGACGAGAGT 7376
QY 9209 TTTATTTACGTTGATATATATAGACAGTCAAGCGGTGCCGTGATATCAGAGACGCGG 9268
Db 7377 TTTATTTACGTTGATATATATAGACAGTCAAGCGGTGCCGTGATATCAGAGACGCGG 7436
QY 9269 TGCCTTAATAGAGATCCGACAGAGCGACAGCATCTTCACTGTCTAGACAGGAGATAT 9328
Db 7437 TGCCTTAATAGAGATCCGACAGAGCGACAGCATCTTCACTGTCTAGACAGGAGATAT 7496
QY 9329 CCGCACCGCTTCCTGTCAGACCCCGAGAGACAGTACCGACCCCTAGCGCGCGGCGCT 9388
|||||

7497 CGCACCGCTTCTGTACGCCCCCGAGGAACAGTACCGACCCCTAGCGCGGCGCCT 7556
QY 9389 ACTGCGCGGAGAAAGCAAAATTAACGGCGTGTGAGAGATCTAGACCTTTAGAGAA 9448
Db 7557 ACTGCGCGGAGAAAGCAAAATTAACGGCGTGTGAGAGATCTAGACCTTTAGAGAA 7616
QY 9449 CCGTGCAGGCGGGCAACAAATGGCCAGGAACTGCGAGCATTTATACGCCAGCTGTGCG 9508
Db 7617 CCGTGCAGGCGGGCAACAAATGGCCAGGAACTGCGAGCATTTATACGCCAGCTGTGCG 7676
QY 9509 CCGTGCAGGCTGAGT 9568
Db 7677 CCGTGCAGGCTGAGT 7736
QY 9569 CATTCTAAAAACAAAAACAGATAGAGAACCTGAACCGCGACCTTCTCGCTGTACG 9628
Db 7737 CATTCTAAAAACAAAAACAGATAGAGAACCTGAACCGCGACCTTCTCGCTGTACG 7796
QY 9629 CGAGCAAACTCGGTAGAGACGTCCAGCGCTGTGCTGAAAGTGGACACCTGGCCAAA 9688
Db 7797 CGAGCAAACTCGGTAGAGACGTCCAGCGCTGTGCTGAAAGTGGACACCTGGCCAAA 7856
QY 9689 CATGAGAGCAAACTCGGGAGCTGGAGGCGAGTCTGGGCAAGATATTGACGCGAGA 9748
Db 7857 CATGAGAGCAAACTCGGGAGCTGGAGGCGAGTCTGGGCAAGATATTGACGCGAGA 7916
QY 9749 GCATTTTGAACACTACCTGAGACCCGAAATGTCACTATCACTACGTTACTTTTCA 9808
Db 7917 GCATTTTGAACACTACCTGAGACCCGAAATGTCACTATCACTACGTTACTTTTCA 7976
QY 9809 GTTTTGGGGGGGGTTAATAGATGTAAACATGTCCCTAATTAACAGATGTGAAGTGT 9868
Db 7977 GTTTTGGGGGGGGTTAATAGATGTAAACATGTCCCTAATTAACAGATGTGAAGTGT 8036
QY 9869 GTGTAAAGACTAGGAGTGTGTATTGTATGTATGTATGTATGTATGTATGTATGTAT 9928
Db 8037 GTGTAAAGACTAGGAGTGTGTATTGTATGTATGTATGTATGTATGTATGTATGTAT 8096
QY 9929 GAACCGGTTCTGACCTTCTGTCAACACTGCGGGGTATCTCCCGATCCGACCCAGA 9988
Db 8097 GAACCGGTTCTGACCTTCTGTCAACACTGCGGGGTATCTCCCGATCCGACCCAGA 8156
QY 9989 CCTATACGTACAGTCACTGCTTGGGTACAGTGTCTGTGAGGAAATCGAATCTGTACAA 10048
Db 8157 CCTATACGTACAGTCACTGCTTGGGTACAGTGTCTGTGAGGAAATCGAATCTGTACAA 8216
QY 10049 TCAGGGGCTCAGTTTACTGCGGCTGTGTGACAGACGACACTCGATCACTCTGTAAAG 10108
Db 8217 TCAGGGGCTCAGTTTACTGCGGCTGTGTGACAGACGACACTCGATCACTCTGTAAAG 8276
QY 10109 GGTAGGGGGAACCAATACAGCGGCTGTTTGAAGACAGAACTGAGCCAGCTGGTCTAAA 10168
Db 8277 GGTAGGGGGAACCAATACAGCGGCTGTTTGAAGACAGAACTGAGCCAGCTGGTCTAAA 8336
QY 10169 AGTAACAAAACGTTGGGAGCCAGCGAGCGGCTGCGCTGTGAGATCACTTAAG 10228
Db 8337 AGTAACAAAACGTTGGGAGCCAGCGAGCGGCTGCGCTGTGAGATCACTTAAG 8396
QY 10229 GAGTGTGCTGCGGGGCGCATACAGATCACTAATTTATCAAAAGGCTGCCGCTCAAT 10288
Db 8397 GAGTGTGCTGCGGGGCGCATACAGATCACTAATTTATCAAAAGGCTGCCGCTCAAT 8456
QY 10349 CGAAAAAGAGTCTACAAATGGCCAGACTGTTAAACACAGAGCGGATATGACAGACCA 10408
Db 8517 CGAAAAAGAGTCTACAAATGGCCAGACTGTTAAACACAGAGCGGATATGACAGACCA 8576
QY 10409 CCGTGCAGTAAATACACCAAACTAAGCGCGATCTACCTTACAGCTGTTCGCGACGGA 10468
Db 8577 CCGTGCAGTAAATACACCAAACTAAGCGCGATCTACCTTACAGCTGTTCGCGACGGA 8636
|||||

QY	112349	GGGCGTGGGTCGTGATATATCGGCATGGCCAGCCGGCGGTGCGCAAAACGTCACACCCCA	11806
Db	9717	GGGCGTGGGTCGTGATATATCGCATGGGCAACGGCGGTTGGCGAAAACGTCACACCCCA	9776
QY	11609	AGGGCGGACACACACCGCGGAACCCAAAGCGCGGGCGCGTCGACGGCCACACCTCCCGGAA	11668
Db	9777	AGGGCGGACACACACCGCGGAACCCAAAGCGCGGGCGCGTCGACGGCCACACCTCCCGGAA	9836
QY	11669	ACCCACCTTAGGGCGGAGAGCGCTTTAAAGTTTCGCTGTGTGACAGCGCTTCGGCCACCGGGAAC	11728
Db	9837	ACCCACCTTAGGGCGGAGAGCGCTTTAAAGTTTCGCTGTGTGACAGCGCTTCGGCCACCGGGAAC	9896
QY	11729	TCCTTCAGGTTTAACTCTGGAAAAAAGCGTTCGGGGCAACCGAGCAAGACGCACCAAGAAG	11788
Db	9897	TCCTTCAGGTTTAACTCTGGAAAAAAGCGTTCGGGGCAACCGAGCAAGACGCACCAAGAAG	9956
QY	11789	GCATCCGATGGGTGTTTAAAAAAAATATTTGCTCCCGCAACATCTTAAAGTTCACAGCGTTAC	11848
Db	9957	GCATCCGATGGGTGTTTAAAAAAAATATTTGCTCCCGCAACATCTTAAAGTTCACAGCGTTAC	10016
QY	11849	GCAAGGTGGCCACCTCGGTGACCGCTCATATGAGAGGTGGAGCCGAGACCGCGCTGACCGGCA	11908
Db	10017	GCAAGGTGGCCACCTCGGTGACCGCTCATATGAGAGGTGGAGCCGAGACCGCGCTGACCGGCA	10076
QY	11909	AGCAAGAGGTATCCGACCGCGTCCGACGTAGAGATCAACACACATGACACGACCTTACC	11968
Db	10077	AGCAAGAGGTATCCGACCGCGTCCGACGTAGAGATCAACACACATGACACGACCTTACC	10136
QY	11969	AGTGTTCACGCTCATCGCGGTAAAGGTCAAGGGGCATAGTAAACACTTCACAGGACAGG	12028
Db	10137	AGTGTTCACGCTCATCGCGGTAAAGGTCAAGGGGCATAGTAAACACTTCACAGGACAGG	10196
QY	12029	ACTTCACCTAACACAGACCGGTGTTTCTGCAACCGGTGCGAGGGGCTCACGATTAACATCCAC	12088
Db	10197	ACTTCACCTAACACAGACCGGTGTTTCTGCAACCGGTGCGAGGGGCTCACGATTAACATCCAC	10256
QY	12089	GATACCTTCAGTCAGCCGGTCTGTACACACACACCGGGATGTGTTCCGGGAATTTACAGGG	12148
Db	10257	GATACCTTCAGTCAGCCGGTCTGTACACACACACCGGGATGTGTTCCGGGAATTTACAGGG	10316
QY	12149	TCACAACACAGGTCATATGCGAATCGTGGACATATGATTCGGCGGCTTGGCGGGAACGCTACT	12208
Db	10317	TCACAACACAGGTCATATGCGAATCGTGGACATATGATTCGGCGGCTTGGCGGGAACGCTACT	10376
QY	12209	CGTATTTTGTTCACCGCCCTGGGAGACACGGTAGAGGTGTCCCGGTTCTGCCAACAGCT	12268
Db	10377	CGTATTTTGTTCACCGCCCTGGGAGACACGGTAGAGGTGTCCCGGTTCTGCCAACAGCT	10436
QY	12269	CAACGTGCTGGGTGGCGGAAAAACGAAACCGGCTCGGGCGCCGCTGTCTACCAATT	12328
Db	10437	CGAGGTGCTGGGTGGCGGAAAAACGAAACCGGCTCGGGAGTCCCGGCGCTACCAAAAT	10496
QY	12329	ACACATTCGTGATTTGGGACCGGACCCGACACACGAAAGCGGGTCTTCCGCGACT	12388
Db	10497	ACACATTCGTGATTTGGGACCGGACCCGACACACGAAAGCGGGTCTTCCGCGACT	10556
QY	12389	CGGAGAGATACACCGTATCGTGGAAAGCGGAGGACCCCAAGTCGGCGGTCTGGCGCTGA	12448
Db	10557	CGGAGAGATACACCGTATCGTGGAAAGCGGAGGACCCCAAGTGGCGGTCTGGCGCTGA	10616
QY	12449	CGCTCTGGAAAAACCTTCCCAAGGCGCATATAGACAGACGACGAGGGCGACTTACACTTGG	12508
Db	10617	CGCTCTGGAAAAACCTTCCCAAGGCGCATATAGACAGACGACGAGGGCGACTTACACTTGG	10676
QY	12509	TGGCGAACGAGTACGCGGACCTTCACGTTCGCCGCTCTCCAGTATACATTTCCACG	12568
Db	10677	TGGCGAACGAGTACGCGGACCTTTTACATCCCGCTCTCCAGTATGGCCACTTTACGG	10736
QY	12569	GCACGTACCCCTGCCTCATATGATGTTATTCAGAAAAACCTCAAGCCGACCATTCAGAGC	12628
Db	10737	GCACGTACCCCTGCCTCATAGAGGTATTTAGAAAAACCTTACAGCACCATTTAAAAAGC	10796
QY	12629	TGTCCTGATACCCACGTCAACAGAGGATGTCGAGATGTAACGAAACCTGACAGACCGGCGTCTCT	12688

Db 10797 TGTCTGATACACATGTGACAAACGGGTGGCCGCTACTTACAGACAGAAAGGGGGCGT 10856
Oy 12689 TTCTCTGTGTGGACCCGTTAAAGCGCGCTTAAGCCTAGTCAGAGATGGCGCAATTAACG 12748
Db 10857 TTCTACTGTGGACCGGTTAAAGCCCTTGAGCCTGTGTTGAGGAATGGCGGCTTAACG 10916
Oy 12749 GCACACGCCAGACACCCGCCACACAACTCAACCGCCACACCGGCTTGAAGAAGCGTCG 12808
Db 10917 GCACACGCCAGACACCCGCCACACTCACTCAACCGTCAGCGGCTTGTGAAGTGTGA 10976
Oy 12809 GTACGAACGAGCAGCAACGAGACACCTAGAGCGGCCCCCACTGAGTGTCCCTAGACA 12868
Db 10977 ATAGGAAGGAGCAGCAACCTAGACACTTGTGAGCGCCCACTGAGTGTCCCTAGACA 11036
Oy 12869 AGCTCCGCGGAGCATCAACAAAGTGTGAGAGACTCTCCAGGGCGTGTGCGGAGAAC 12928
Db 11037 AACTACGCGGAGCATCAACAAAGTGTGAGAGAACTCCAGGGCGTGTGCGGAGAAC 11096
Oy 12929 AGGTGAGGAGACACTATGATGTGTAGCAACTGAGCAAGATTAAACCCACAGCGTAATGA 12988
Db 11097 AGGTGAGGAGACACTATGATGTGTAGCAACTGAGCAAGATTAAACCCACAGCGTAATGA 11156
Oy 12989 CGGCGATATACGGGCGCGGTGTGCGCAAGTTCGTGGGGAGCGCATGTCGCTGACGG 13048
Db 11157 CAGGATATACGGGCGCGGTGTGCGCAAGTTCGTGGGGAGCGCATGTCGCTGACAG 11216
Oy 13049 ACTGCTGGCGGTGAGACAGGCGTCCGTACAGCATCAACAAAGCCTCCGACGTCACCC 13108
Db 11217 ACTGCTGGCGGTGAGACAGGCGTCCGTACAGCATCAACAAAGCCTCCGACGTCACCC 11276
Oy 13109 CGGGATCTGCTACTTCGCGCCCGCGGTCAAGTTCAGTTCCTCTAACAGCACCGCTGT 13168
Db 11277 CGGGAATGTGCTACTTCGCGCCCGCGGTCAAGTTCAGTTCCTCTAACAGCACCGCTGT 11336
Oy 13169 TCAAGGGCCAGCTGGGAGCCAGAAAGAGATCATCTAGAGAGACAAACAGGTGGAGGCGT 13228
Db 11337 TCAAGGGCCAGCTGGGAGCCAGAAAGAGATCATCTAGAGAGACAAACAGGTGGAGGCGT 11396
Oy 13229 GCAAGAGACGTGCGAACACTACTTCTATAGCAGCAACGTAACCTACTACTACAAAGACT 13288
Db 11397 GCAAGAGACGTGCGAACACTACTTCTATAGCAGCAACGTAACCTACTACTACTACAAAGACT 11456
Oy 13289 ACGTCTCGTGAAGAAATTAACACCTCGAGATATCCACCTCGGAGCTTCATCGCCC 13348
Db 11457 ACGTCTCGTGAAGAAATTAACACCTCGAGATATCCACCTCGGAGCTTCATCGCCC 11516
Oy 13349 TGAACCTGTGTTATAGAGAACATAGATTTCAGGGTCAATGAGGGAATTAACACTACT 13408
Db 11517 TGAACCTGTGTTATAGAGAACATAGATTTCAGGGTCAATGAGGGAATTAACACTACT 11576
Oy 13409 AGAAGAAAGCTGTCCGGGAGCGTTTGTGATATAGAAACCATGTTGAGGGAATTAACACTACT 13468
Db 11577 AGAAGAAAGCTGTCCGGGAGCGTTTGTGATATAGAAACCATGTTGAGGGAATTAACACTACT 11636
Oy 13469 ACACGCAACGCTGGGGGAGCTCGGGAGAGACTGGAGCAACAGATGCAACCTCAACCGCG 13528
Db 11637 ACACGCAACGCTGGGGGAGCTCGGGAGAGACTGGAGCAACAGATGCAACCTCAACCGCG 11696
Oy 13529 ACCGCTGGCCCGAGACTGTCCGAGATAGTCGCGAGCTGGGAGATGTCGCGGACGG 13588
Db 11697 ACCGCTGGCCCGAGACTGTCCGAGATAGTCGCGGAGCTGGGAGATGTCGCGGACGG 11756
Oy 13589 TCGTTAAAGTGGCCAGTACGCTGATTAACCTGTTGCGATCAATCGTAGCGGGTTCAATTA 13648
Db 11757 TCGTTAAAGTGGCCAGTACGCTGATTAACCTGTTGCGATCAATCGTAGCGGGTTCAATTA 11816
Oy 13649 ACTTTAAAGATTCGCTTCGGGGGAGATGCTATGATCCCTGCGATTTGGCGGCTGTCC 13708
Db 11817 ACTTTAAAGATTCGCTTCGGGGGAGATGCTATGATCCCTGCGATTTGGCGGCTGTCC 11876
Oy 13709 TGAATCGTGTTCGCTTAACCGGCGCACCAACCGCATCGCCAGGCGCCCATCAGATGA 13768
|||||

Db 11877 TGAATCGTGTTCGCTTAACCGGCGCACCAACGCCATCGCCAGGCCCCCATCAGATGA 11936
Oy 13769 TCTACCCCGACATATAGACAAATGACAGCCCTCTGTGGCGGTAAAGTGCAGACAGACAGATTA 13828
Db 11937 TCTACCCCGACATATAGACAAATGACAGCCCTCTGTGGCGGTAAAGTGCAGACAGACAGATTA 11996
Oy 13829 AAAACATTCGCGCGGATGACACAGCTACAGCAGAGAAAGCGTAGCGGTTAGAGCAAC 13888
Db 11997 AAAACATTCGCGCGGATGACACAGCTACAGCAGAGAAAGCGTAGCGGTTAGAGCAAC 12056
Oy 13889 AGCAGAGGTACAGCGCCCTCTGCTTTTCGGGGCGGTGACAGAGGACTTAAGTAAAGTGGCTTTA 13948
Db 12057 AGCAGAGGTACAGCGCCCTCTGCTTTTCGGGGCGGTGACAGAGGACTTAAGTAAAGTGGCTTTA 12116
Oy 13949 GGGGATATTAACCGCTGGAAGAGAGGCTCAAGAGTATGAATGAGCAATTAACAC 14008
Db 12117 GGGGATATTAACCGCTGGAAGAGAGGCTCAAGAGTATGAATGAGCAATTAACAC 12176
Oy 14009 ACCCACACGCTGTACTTGGCCGCCAGAGCCCGGCGCAATGATTCGCGCACCCG 14068
Db 12177 ACCCACACGCTGTACTTGGCCGCCAGAGCCCGGCGCAATGATTCGCGCACCCG 12236
Oy 14069 GCGGTCGCCGACACCTTAAGGCGCCCGGGGGTCCGGGCTGTATCAATCATGATTT 14128
Db 12237 GCGGTCGCCGACACCTTAAGGCGCCCGGGGGTCCGGGCTGTATCAATCATGATTT 12296
Oy 14129 TCTTTAACCCGTAACCTGAGGCGCTTGCAGACAGCCGCCCACTACACAGAGCAGCAGATG 14188
Db 12297 TCTTTAACCCGTAACCTGAGGCGCTTGCAGACAGCCGCCCACTACACAGAGCAGCAGATG 12356
Oy 14189 CTCGCGCGCTGCGCGGCGCGGAGCGCTTACGCGCCACACAGAGCTTTGAGGCTCATCC 14248
Db 12357 CTCGCGCGCTGCGCGGCGCGGAGCGCTTACGCGCCACACAGAGCTTTGAGGCTCATCC 12416
Oy 14249 CCGCCTGCTCCGACAGCCGAGGGGAGGGGAGTGAATCCGGTACAGATCCGTTCCCGG 14308
Db 12417 CCGCCTGCTCCGACAGCCGAGGGGAGGGGAGTGAATCCGGTACAGATCCGTTCCCGG 12476
Oy 14309 CAACGTACTTGAAGAACGCTGTCGCGGAGACGTGCTCGCCCAAGCAATCATCAGCTTTC 14368
Db 12477 CAACGTACTTGAAGAACGCTGTCGCGGAGACGTGCTCGCCCAAGCAATCATCAGCTTTC 12536
Oy 14369 GGAAGCGCGCGGAGCCGCAAGCCGTCGCGCCCGGAGCCCAAGCAATCATCAGCTTTC 14428
Db 12537 GGAAGCGCGCGGAGCCGCAAGCCGTCGCGCCCGGAGCCCAAGCAATCATCAGCTTTC 12596
Oy 14429 ACGGTAACGACGTGTTGAAGAACAGCTAGCGGGGAGACAGGTGTGCGGAGTACTAGGCT 14488
Db 12597 ACGGTAACGACGTGTTGAAGAACAGCTAGCGGGGAGACAGGTGTGCGGAGTACTAGGCT 12656
Oy 14489 GCTTCCAAACGACATTAATCCCAAGCGGAACCGTGTCAAGCTCTGGGGCGAACCAGAG 14548
Db 12657 GCTTCCAAACGACATTAATCCCAAGCGGAACCGTGTCAAGCTCTGGGGCGAACCAGAG 12716
Oy 14549 ACGGCAACGAGCGTGTGGAAGTGTCCGTCACAAAGTATATTTCTACGGAAGGTTTC 14608
Db 12717 ACGGCAACGAGCGTGTGGAAGTGTCCGTCACAAAGTATATTTCTACGGAAGGTTTC 12776
Oy 14609 CAGCGCGATTAACGTCACCCACATCTCCAGAGGCGCTCAAGAAACACAGCGCGGCGGTG 14668
Db 12777 CAGCGCGATTAACGTCACCCACATCTCCAGAGGCGCTCAAGAAACACAGCGCGGCGGTG 12836
Oy 14669 CCGCGTGGCGGCTTTCGACAGAGAGTGAACAAAAGATTTCTCAAAAGTACAGAGTGC 14728
Db 12837 CCGCGTGGCGGCTTTCGACAGAGAGTGAACAAAAGATTTCTCAAAAGTACAGAGTGC 12896
Oy 14729 CGGAGATCCGTCACAGGAAATCAGGCTATCGTCCGGTTCCATGCTCTGACACCTCAGCG 14788
Db 12897 CGGAGATCCGTCACAGGAAATCAGGCTATCGTCCGGTTCCATGCTCTGACACCTCAGCG 12956
Oy 14789 ACCGCTGCTGCGGCGGCGGTGAGAGTGTGAGTCAAAAGTGAAGCGCGGCTTCCCGGT 14848
Db 12957 ACCGCTGCTGCGGCGGCGGTGAGAGTGTGAGTCAAAAGTGAAGCGCGGCTTCCCGGT 13016
|||||

QY 14849 TCGTTCGATCAACGGGTTTACACGCTTCGGGTGGTACTGTGCGCGCGCCAGCCCC 14908
D 13017 TCGTTCGATCAACGGGTTTACACGCTTCGGGTGGTACTGTGCGCGCGCCAGCCCC 13076
QY 14909 GCGTCGGCGGACAGATGCGACGAGCGGCTTGAGATTTGACTGAGTGGAGAGCTCA 14968
D 13077 GCGTCGGCGGACAGATGCGACGAGCGGCTTGAGATTTGACTGAGTGGAGAGCTCA 13136
QY 14969 GCGTCGAAGGGAGCCGAGGAGCTGCGCCCGTACCGCATCGTGGCTTTGATTCGAGT 15028
D 13137 GCGTCGAAGGGAGCCGAGGAGCTGCGCCCGTACCGCATCGTGGCTTTGATTCGAGT 13196
QY 15029 GCACGTGAGAGGCGGATTTCCGTGCGCACGCGCGACGCGGATCCAGATCT 15088
D 13197 GCACGTGAGAGGCGGATTTCCGTGCGCACGCGCGACGCGGATCCAGATCT 13256
QY 15089 CCGTCGCTCTTACACGACGAGGAGGCGGCCCAATCCGCCAATCTGTTACGCG 15148
D 13257 CCGTCGCTCTTACACGACGAGGAGGCGGCCCAATCCGCCAATCTGTTACGCG 13316
QY 15149 TCGGGAGGTGCGACCCGATCCCGGACGCGAGCTTTGAGTTCCGTGGGAATATGACA 15208
D 13317 TCGGGAGGTGCGACCCGATCCCGGACGCGAGCTTTGAGTTCCGTGGGAATATGACA 13376
QY 15209 TCGTGTGTGCTCTTCCGATGATCCGCGACTTCGAGGTGAGACTTTTAAACCGGCTATA 15268
D 13377 TCGTGTGTGCTCTTCCGATGATTCGCGACTTCGAGGTGAGACTTTTAAACCGGCTATA 13436
QY 15269 ACATCTCAAACTTCGATCTCCCGTACTTAATCACGCGAGCGTCCAGAGTGTACAACCTTC 15328
D 13437 ACATCTCAAACTTCGATCTCCCGTACTTAATCACGCGAGCGTCCAGAGTGTACAACCTTC 13496
QY 15329 GATTAAAGCATACAAAAATAAAACCGGCTCATCTTGAAGTTACAGAGCCCGGTG 15388
D 13497 GATTAAAGCATACAAAAATAAAACCGGCTCATCTTGAAGTTACAGAGCCCGGTG 13556
QY 15389 GCGGGGAGGGGGGTTTCATGAGGTGCGTCTCAAAAAATTAATTAAGCGGATCCGCCCA 15448
D 13557 GCGGGGAGGGGGGTTTCATGAGGTGCGTCTCAAAAAATTAATTAAGCGGATCCGCCCA 13616
QY 15449 TAGACATGTACACAGGTGTGTCGCGAAAAAGCTCAACCTTCGCGATACAACTGGACACGG 15508
D 13617 TAGACATGTACACAGGTGTGTCGCGAAAAAGCTCAACCTTCGCGATACAACTGGACACGG 13676
QY 15509 TGGCGAGGCAGTGTCTGGGTGGGAAAAAGAGAGCTATGTACAAAGACATTCGCCCTC 15568
D 13677 TGGCGAGGCAGTGTCTGGGTGGGAAAAAGAGAGCTATGTACAAAGACATTCGCCCTC 13736
QY 15569 TGTTCGCTAGGTCCGCGGGGACGAGGCTAAGGTGAGGCTATTCGCTGATGAGCTCGG 15628
D 13737 TGTTCGCTAGGTCCGCGGGGACGAGGCTAAGGTGAGGCTATTCGCTGATGAGCTCGG 13796
QY 15629 TCTGTGTAGTGAACCTTTAAAAATGTTATGATATACAGTGGAGATTTCCGAGATACCA 15688
D 13797 TCTGTGTAGTGAACCTTTAAAAATGTTATGATATACAGTGGAGATTTCCGAGATACCA 13856
QY 15689 AGCTGGCAAGATTCAGGCGAGCGGCTCTGACGAGCGGCAACACCTCCGCTGTCT 15748
D 13857 AGCTGGCAAGATTCAGGCGAGCGGCTCTGACGAGCGGCAACACCTCCGCTGTCT 13916
QY 15749 CCGTCGCTGAGAGCGCGCGGACGAGGAGAACTTTATCTCCGCTTCCAAAGCGCCGAGG 15808
D 13917 CCGTCGCTGAGAGCGCGCGGACGAGGAGAACTTTATCTCCGCTTCCAAAGCGCCGAGG 13976
QY 15809 GACAGGGGGGCTATCAGGGCGGACGAGTATCAACCCATTCGCGGGTTTTACGAGAGC 15868
D 13977 GACAGGGGGGCTATCAGGGCGGACGAGTATCAACCCATTCGCGGGTTTTACGAGAGC 14036
QY 15869 CGGTCTGTGTGTGATTTTTCAGCTGTATCCGAGACATCATCCAGGCGCAACCTGT 15928
D 14037 CGGTCTGTGTGTGATTTTTCAGCTGTATCCGAGACATCATCCAGGCGCAACCTGT 14096

QY 15929 GCTACTCCACCATGATATACAGGAGAGACCTGCAACCTGCAACCCCAACCTGACCGGACG 15988
D 14097 GCTACTCCACCATGATATACAGGAGAGACCTGCAACCTGCAACCCCAACCTGACCGGACG 14156
QY 15989 ACTACGAGAGCTTCGTCTACGCGGCGGACCGGTACATTTTGTAAAAAACACAGCGGG 16048
D 14157 ACTACGAGAGCTTCGTCTACGCGGCGGACCGGTACATTTTGTAAAAAACACAGCGGG 14216
QY 16049 AGTCTGTGGGGAGAGCTGTAACCGTGTGGTTAGAAAAAGCGAAGGGGCAATCCGGGCA 16108
D 14217 AGTCTGTGGGGAGAGCTGTAACCGTGTGGTTAGAAAAAGCGAAGGGGCAATCCGGGCA 14276
QY 16109 CCGTCGCGGCGGTGCGATGACCCGCTGCTAAAAAACCATCTTATGATTAACAACAGCTGGCA 16168
D 14277 CCGTCGCGGCGGTGCGATGACCCGCTGCTAAAAAACCATCTTATGATTAACAACAGCTGGCA 14336
QY 16169 TCAAGGTGACATGTATACCGGTTTACGGGTTTACCGGGGTGCGGAGCGGCTCTCCAT 16228
D 14337 TCAAGGTGACATGTATACCGGTTTACGGGTTTACCGGGGTGCGGAGCGGCTCTCCAT 14396
QY 16229 GCATTTACATAGCGGAAACCGTGAAGCTCCGCGGGGCGCACGATGCTGAGATGTCAAGT 16288
D 14397 GCATTTACATAGCGGAAACCGTGAAGCTCCGCGGGGCGCACGATGCTGAGATGTCAAGT 14456
QY 16289 CTTACGTGAGGCGCTGACGACGAGAACCTGCGAACGCTCTCGTCCGAGGTGACCG 16348
D 14457 CTTACGTGAGGCGCTGACGACGAGAACCTGCGAACGCTCTCGTCCGAGGTGACCG 14516
QY 16349 CCGGTACAGGCGCGGCTTTCCGCTGCTTACGCTGACACCGACTCCCTTTATCGCGT 16408
D 14517 CCGGTACAGGCGCGGCTTTCCGCTGCTTACGCTGACACCGACTCCCTTTATCGCGT 14576
QY 16409 GCGAGCGTTATTCGCGGAAAGCGGTTCCGTTTCTGTGAGATCTGCGCGCGAGATCA 16468
D 14577 GCGAGCGTTATTCGCGGAAAGCGGTTCCGTTTCTGTGAGATCTGCGCGCGAGATCA 14636
QY 16469 CTGCGGACCTGTTCCGCCCAACCCATTAAGCTAGAGGCGGAAAGACGTTCAAGTGTGCG 16528
D 14637 CTGCGGACCTGTTCCGCCCAACCCATTAAGCTAGAGGCGGAAAGACGTTCAAGTGTGCG 14696
QY 16529 TGTGTGTGACGAAAAACGCTTACTGCGGCTCTTATGAAACGACAAAAATGCTATGAAG 16588
D 14697 TGTGTGTGACGAAAAACGCTTACTGCGGCTCTTATGAAACGACAAAAATGCTATGAAG 14756
QY 16589 GGGTCGACCTCATTCGCGAAAAACGCGTGCAGAACTTGTCCAGAGACGATGCGCGCCATTC 16648
D 14757 GGGTCGACCTCATTCGCGAAAAACGCGTGCAGAACTTGTTCAGAGACGATGCGCGCCATTC 14816
QY 16649 TGGACCTGTGTCTCCAGATCCGAGAGTCAAGGCTGCGGCGCGGCTGTTGTCAAGCGGC 16708
D 14817 TGGACCTGTGTCTCCAGATCCGAGAGTCAAGGCTGCGGCGCGGCTGTTGTCAAGCGGC 14876
QY 16709 CGCCGACGCGGTTATACGAGAGGCGCTGCCGCTGCTTTATAAAAATCGTAGAGTCC 16768
D 14877 CGCCGACGCGGTTATACGAGAGGCGCTGCCGCTGCTTTATAAAAATCGTAGAGTCC 14936
QY 16769 TCAAGGAGAGCTATCTGAGACTCCGAAAAACGCGTGGCCATGAGACAGATTAAGTTCT 16828
D 14937 TCAAGGAGAGCTATCTGAGACTCCGAAAAACGCGTGGCCATGAGACAGATTAAGTTCT 14996
QY 16829 CCACCGAGCTCAGCGCGCGGCTGCGATTACAAAGACCAACCTGCCCACTGGCGG 16888
D 14997 CCACCGAGCTCAGCGCGCGGCTGCGATTACAAAGACCAACCTGCCCACTGGCGG 15056
QY 16889 TGTACAAAAAGCTTGCGACGAGTGGCAGAGACTGCCCAAGTGCACGATATGAAATCCCT 16948
D 15057 TGTACAAAAAGCTTGCGACGAGTGGCAGAGAGCTGCCCAAGTGCACGATATGAAATCCCT 15116
QY 16949 ACGTGTCTGTTGAGCGCGCGGCTCTAAAGTGTGGAAGCTGGCGGCAACCCGATTAAG 17008
D 15117 ACGTGTCTGTTGAGCGCGCGGCTCTAAAGTGTGGAAGCTGGCGGCAACCCGATTAAG 15176
QY 17009 TCAACAGACACAGATTCGCGGTGCGACTATATTTTCGACAAACTGGTGCACGCGG 17068

|||||
Db 15177 TCAGACGACACGATTCCTCGGCTGACCTATATTTTCAGAACTGTGTACGGCG 15236
QY 17069 CGGCGCAACATCTCTCACTGTCTGTTCGGCAACAACGGGAGACACACGATGGCCATCTCT 17128
Db 15237 CGGCGCAACATCTCTCACTGTCTGTTCGGCAACAACGGGAGACACACGATGGCCATCTCT 15296
QY 17129 ACAATTTTCTCAACGTCCTGATTAAGCTGTTCGTGTGACGCCAATTTGAGAACGCCAAC 17188
Db 15297 ACAATTTTCTCAACGTCCTGATTAAGCTGTTCGTGTGACGCCAATTTGAGAACGCCAAC 15356
QY 17189 ATAGAAGCGCGCGCAGCGGAGTCCGAGGAGAGAGCTCGAGGGCGAGCGGAGCGACCAACG 17248
Db 15357 ATAGAAGCGCGCGCGCAGCGGAGTCCGAGGAGAGAGCTCGAGGGCGAGCGGAGCGACCAACG 15416
QY 17249 GAGACCGCCACATGCTGTGTTAAAGAACTGTCTGCTGCTCGGCGACTGCGAGGTGACT 17308
Db 15417 GAGACCGCCACATGCTGTGTTAAAGAACTGTCTGCTGCTCGGCGACTGCGAGGTGACT 15476
QY 17309 TTTTACCGGGGGTGAATTCAGCTTCGTCACCTTACCCGCTGCAAAAGTTCAAGGGCCAC 17368
Db 15477 TTTTACCGGGGGTGAATTCAGCTTCGTCACCTTACCCGCTGCAAAAGTTCAAGGGCCAC 15536
QY 17369 GGGGGCTAGCGCAGGGGTCGACCTCCCTTCTGCTGACCAAGTTACCTCACCAACATTTTC 17428
Db 15537 GGGGGCTAGCGCAGGGGTCGACCTCCCTTCTGCTGACCAAGTTACCTCACCAACATTTTC 15596
QY 17429 GCGTTGCGACTCTGACGCGCTCTCAAGAACTGCCCCCTTCTCCGACTGCTGCGCCCTT 17488
Db 15597 GCGTTGCGACTCTGACGCGCTCTCAAGAACTGCCCCCTTCTCCGACTGCTGCGCCCTT 15656
QY 17489 ATGCGCCCGTTGATTCGCGCGCGCGACCGGAGAGCGGCGCGCTGGCCCGCGGGTTCGTG 17548
Db 15657 ATGCGCCCGTTGATTCGCGCGCGCGACCGGAGAGCGGCGCGCTGGCCCGCGGGTTCGTG 15716
QY 17549 CTGAGACTCTCTGCGCGCTGACCGTGTGGGTAAAGCGGAGCGGCGCGACACGATCCGG 17608
Db 15717 CTGAGACTCTCTGCGCGCTGACCGTGTGGGTAAAGCGGAGCGGCGCGACACGATCCGG 15776
QY 17609 TTTTGCCTCTCTTTTAAAGCCGATGACCTGTGAGCGCGCGGTTCACGTACTTTCGGC 17668
Db 15777 TTTTGCCTCTCTTTTAAAGCCGATGACCTGTGAGCGCGCGGTTCACGTACTTTCGGC 15836
QY 17669 GAGAAAGCGGCGCGCGCTCGGAGGAGCGGCGGACCCCAACCTGCGCGGACCGGAAACCTG 17728
Db 15837 GAGAAAGCGGCGCGCGCTCGGAGGAGCGGCGGACCCCAACCTGCGCGGACCGGAAACCTG 15896
QY 17729 CCGGCTGAGACCCCTGCGCTCTCCGCGAGGCGTCTCAGACGTGCGCCCATTTCTTCGT 17788
Db 15897 CCGGCTGAGACCCCTGCGCTCTCCGCGAGGCGTCTCAGACGTGCGCCCATTTCTTCGT 15956
QY 17789 GCGTATTTTCCACGCGGCACTGGTGGCTGCTTAAGCTGTTCGGGTTCACGTGAGG 17848
Db 15957 GCGTATTTTCCACGCGGCACTGGTGGCTGCTTAAGCTGTTCGGGTTCACGTGAGG 16016
QY 17849 CCGTTTTCGATGAGCGGCGGAGACAGGAGGCGGCGGATCTCCCGGAAATACGTCACGTTT 17908
Db 16017 CCGTTTTCGATGAGCGGCGGAGACAGGAGGCGGCGGATCTCCCGGAAATACGTCACGTTT 16076
QY 17909 AGTAATCTCCGGGGGTAACTGTGCAAGGCGCTGCTTACACGCTGTCGCCGTCGCGGT 17968
Db 16077 AGTAATCTCCGGGGGTAACTGTGCAAGGCGCTGCTTACACGCTGTCGCCGTCGCGGT 16136
QY 17969 AAAACGCGCAATGGAATCTATCTACGCTCCCGGGAGCCCAACGCGGAGATAGTCTG 18028
Db 16137 AAAACGCGCAATGGAATCTATCTACGCTCCCGGGAGCCCAACGCGGAGATAGTCTG 16196
QY 18029 GGGCGATCGGAGCGCTCTGCGGACCGGACACCGGCGGCGGTATTTGGGGGTCTACGCC 18088
Db 16197 GGGCGATCGGAGCGCTCTGCGGACCGGACACCGGCGGCGGTATTTGGGGGTCTACGCC 16256
QY 18089 GAGCGCGAAAAACATCCACTGGAAGCTCCGCGGAGTCCGGGTATGTTAATCTTC 18148
|||||

Db 16257 GAGCGCGAAAAACATCCACTGGAAGCTCCGCGGAAGTCCGGGTATGATTATCTTC 16316
QY 18149 CAACAGGAGAGCGCGCTCGGCGGAGTTCGGCTTTCTGTGTCAGCGGCGGTGACCGCGAG 18208
Db 16317 CAACAGGAGAGCGCGCTCGGCGGAGTTCGGCTTTCTGTGTCAGCGGCGGTGACCGCGAG 16376
QY 18209 CCGCTATTCGTCTCACCCCGGACGCTTTCGTTTCGGTTGCAACCAACCTGCGCTA 18268
Db 16377 CCGCTATTCGTCTCACCCCGGACGCTTTCGTTTCGGTTGCAACCAACCTGCGCTA 16436
QY 18269 TTCAACCCCAAGGTTACCCCGACGACTATTAAGAGACACCTTGGCGCGCGCGG 18328
Db 16437 TTCAACCCCAAGGTTACCCCGACGACTATTAAGAGACACCTTGGCGCGCGCGG 16496
QY 18329 CCGTGCCTCGGTGCGATTAAGCTCCGCGGACGAGCGCGCGGAGACCTGTCGCTCA 18388
Db 16497 CCGTGCCTCGGTGCGATTAAGCTCCGCGGACGAGCGCGCGGAGACCTGTCGCTCA 16556
QY 18389 CCAGACACCGGGGCGCTCTCATTTAACGCGTTTACATCCCGTCCGTTTCCAGGGGTG 18448
Db 16557 CCAGACACCGGGGCGCTCTCATTTAACGCGTTTACATCCCGTCCGTTTCCAGGGGTG 16616
QY 18449 GTCTGGGGAAGTGTACGAGTCCCTACGCGAACGAGGGGTCCACGAAACGATGAACAT 18508
Db 16617 GTCTGGGGAAGTGTACGAGTCCCTACGCGAACGAGGGGTCCACGAAACGATGAACAT 16676
QY 18509 TGAACGCAACGATGAGAACACCGGTGCTTCTTTCGCGGCGAGTGGAGACCTGAGTTC 18568
Db 16677 TGAACGCAACGATGAGAACACCGGTGCTTCTTTCGCGGCGAGTGGAGACCTGAGTTC 16736
QY 18569 TAGTGGACAACGGGACAGCCAGGTACAGTCCCTGCTGTGTGGGCGCGCATTTACAGACG 18628
Db 16737 TAGTGGACAACGGGACAGCCAGGTACAGTCCCTGCTGTGTGGGCGCGCATTTACAGACG 16796
QY 18629 GCTACCTGACACTGTGGAACAGGTGACAGCTGTGCTACGGAAGAGTTCCTGCTGTC 18688
Db 16797 GCTACCTGACACTGTGGAACAGGTGACAGCTGTGCTACGGAAGAGTTCCTGCTGTC 16856
QY 18689 CCGCATGCCCCAGCATCGGAGAGCTGTGCGGAAGAGTTTCCGGCTTTCGCTTGGCA 18748
Db 16857 CCGCATGCCCCAGCATCGGAGAGCTGTGCGGAAGAGTTTCCGGCTTTCGCTTGGCA 16916
QY 18749 GCGGCACTCTGGGCGATCGGGGACACGACCGGTTCACGCGTTCCGCTCACCGGACA 18808
Db 16917 GCGGCACTCTGGGCGATCGGGGACACGACCGGTTCACGCGTTCCGCTCACCGGACA 16976
QY 18809 ACCCACTGGACATAGTACCAGCGCTGTGTCAGACCGCGGAGTGCAGCTGTGTCGCGG 18868
Db 16977 ACCCACTGGACATAGTACCAGCGCGCTGTGTCAGACCGCGGAGTGCAGCTGTGTCGCGG 17036
QY 18869 TTACGCTCTCGCAACACGCGGCTGTGCGGATACGGACTTAAAGTATTCGTGCGATCG 18928
Db 17037 TTACGCTCTCGCAACACGCGGCTGTGCGGATACGGACTTAAAGTATTCGTGCGATCG 17096
QY 18929 TTACGCTGTGCGCGCGCGCGGGGTTCCTACCTTCCAAACACGCGCTTCGATCG 18988
Db 17097 TTACGCTGTGCGCGCGCGCGGGGTTCCTACCTTCCAAACACGCGCTTCGATCG 17156
QY 18989 CCGTGAACAGCGCTGTCAGACGAGGAGGCTCCAGGCTTAACCTCTAAGAGCGTGGATTA 19048
Db 17157 CCGTGAACAGCGCGTGTGACAGGAGGAGGCTCCAGGCTTAACCTCTAAGAGCGTGGATTA 17216
QY 19049 AAATTCAGGCTTCCCGTCTATCTATGACGAGACGCGCACCATTTCTTTAACCCAGA 19108
Db 17217 AAATTCAGGCTTCCCGTCTATCTATGACGAGACGCGCACCATTTCTTTAACCCAGA 17276
QY 19109 AGACCAAGCCCTTTTACCGAGCAAGTTCGCGGCTGATATGACAAACGACGAGCCGA 19168
Db 17277 AGACCAAGCCCTTTTACCGAGCAAGTTCGCGGCTGATATGACAAACGACGAGCCGA 17336
QY 19169 GCGCGGTAAACACCTCTTACGCGGAAAGACGACGTAAGGTTGACCGTGCACCGCCGCC 19228
Db 17337 GCGCGGTAAACACCGTCTTACGCGGAAAGACGACGTAAGGTTGACCGTGCACCGCCGCC 17396
|||||

QY	19229	CGGAACATCGTACCGAGCGGCCCGGTGACGAGCCGCTGTCCACCGGTAAATGCC	19288
Db	17397	CGGAACAAATCGTACCGAGCGGCCCGGTACGAGCCGCTGTCCACCGGTAAATGCC	17456
QY	19289	CAATCGCCTTTCGCGCAACCCATACTTTGAATCCCGTGTGTCCACACGGGGAAT	19348
Db	17457	CAATCGCCTTTCGCGCAACCCATACTTTGAATCCCGTGTGTGTCCACACGGGGAAT	17516
QY	19349	TCAGGCCCGTGTAGTACGTGGGCGCTACCGTGTGCAATCCACCAACTGTAGCAATTCG	19408
Db	17517	TCAGGCCCGTGTGTAGTGGGCGCTACCGTGTGCAATCCACCAACTGTAGCAATTCG	17576
QY	19409	TAAGTACGGTAAACACTTACGTCTGGCATTTAAACCGCAAGCTGACGGCGATTATTAACA	19468
Db	17577	TAAGTACGGTAAACACTTACGTCTGGCATTTAAACCGCAAGCTGACGGCGATTATTAACA	17636
QY	19469	ATCAGGCCCAACACGGGGGTTCCGGATTCAGGACTGCGAATGTGGCCACCGAACCGGGAGA	19528
Db	17637	ATCAGGCCCAACACGGGGGTTCCGGATTCAGGACTGCGAATGTGGCCACCGAACCGGGAGA	17696
QY	19529	TAGAGATTTTGTATACCAAGTGTCCAGAGCCCGCGGTATACATACAGACCGGGAGCGAGC	19588
Db	17697	TAGAGATTTTGTATACCAAGTGTCCAGAGCCCGCGGTATACATACAGACCGGGAGCGAGC	17756
QY	19589	TGGGGCAAGCCATCTTCGTGTTCGCGCGCGGTTCGTGTGGCCCGGGGAAACTGCGGAGC	19648
Db	17757	TGGGGCAAGCCATCTTCGTGTTCGCGCGCGGTTCGTGTGGCCCGGGGAAACTGCGGAGC	17816
QY	19649	TCCTCGGCCACCGATCGCGCGCCCTGGAGCTGCCGGGGGGGTGACAGTGGACAGCCAAA	19708
Db	17817	TCCTCGGCCACCGATCGCGCGCCCTGGAGCTAACGGGGCGGGGTGACAGTGGACAGCCAAA	17876
QY	19709	AACGTGTAGTTTGAAGACATGTACTGTTTTCACGTAATTTCTAATTAACGGTTTG	19768
Db	17877	AACGTGTAGTTTGAAGACATGTACTGTTTTCACGTAATTTCTAATTAACGGTTTG	17936
QY	19769	CTCGTATCGCTCACACAAAGCCCAAAACGTTCTCATTCCTCGGGGTGCGCGCCTCGCAAA	19828
Db	17937	CTCGTATCGCTCACACAAAGCCCAAAACGTTCTCATTCCTCGGGGTGCGCGCCTCGCAAA	17996
QY	19829	CACCAAGGTGTCTCAAAACACCCCTCCCGCACCCCTCGGCACACAAAACGTTAACGC	19888
Db	17997	CACCAAGGTGTCTCAAAACACCCCTCCCGCACCCCTCGGCACACAAAACGTTAACGC	18056
QY	19889	CTTCGGTGTAGTGTAGTTTATTTATTTATTTATTAATATATGCTATTGCGGGGGCCCG	19948
Db	18057	CTTCGGTGTAGTGTAGTTTATTTATTTATTTATTAATATATGCTATTGCGGGGGCCCG	18116
QY	19949	TCGCCGAAACAACTGTGTAGATATTTCCAGTATGCGAAAGCGCCTGAGAACACGTCGCG	20008
Db	18117	TCGCCGAAACAACTGTGTAGATATTTCCAGTATGCGAAAGCGCCTGAGAACACGTCGCG	18176
QY	20009	GGGCTGTGCCCTCCCAACGACGACGACGATTTTTCATTTAGACTCCGCGCACCTATCTTG	20068
Db	18177	GGGCTGTGCCCTCCCAACGACGACGACGATTTTTCATTTAGACTCCGCGCACCTATCTTG	18236
QY	20069	TTATTTCAGGGAAGTCCTCAATTTAAGATGTCAGGGCGGAGACACCCAGGTACCGCG	20128
Db	18237	TTATTTCAGGGAAGTCCTCAATTTAAGATGTCAGGGCGGAGACACCCAGGTACCGCG	18296
QY	20129	GAGCAATGTGCGGGGCGTCCGGTCCCGGGGCGCTGTCTCAGCAGCATTCCTCAGTGCG	20188
Db	18297	GAGCAATGTGCGGGGCGTCCGGTCCCGGGGCGCTGTCTCAGCAGCATTCCTCAGTGCG	18356
QY	20189	GTCAGGTAACTCTGTAGGCCCGGAGCCCGCGAACCATGGCGTTCTATCACTGTGCGCCG	20248
Db	18357	GTCAGGTAACTCTGTAGGCCCGGAGCCCGCGAACCATGGCGTTCTATCACTGTGCGCCG	18416
QY	20249	CGAAATCTCGGGCGCTGGCACTCAAGTTTAGACATCAATATAGGAAGTGAACAAACGAC	20308
Db	18417	CGAAATCTCGGGCGCTGGCACTCAAGTTTAGACATCAATATAGGAAGTGAACAAACGAC	18476

Qy	20309	ATGATGGCGGGGATACCTACCCACCCGACAGAGATGTGGTGGCACAGTAAACGAC	20368
Db	18477	ATGATGGCGGGGATACCTACCCACCCGACAGAGATGTGGTGGCACAGTAAACGAC	18536
Qy	20369	CAGGCGTGTATGTTTAACCCACTTACAGACAGCGCCCTGTGCTGTCAAGAGAGCG	20428
Db	18537	CAGGCGTGTATGTTTAACCCACTTACAGACAGCGCCCTGTGCTGTCAAGAGAGCG	18596
Qy	20429	CGTTTGCCCGCCACTGGGGGAGACGTTAAATTCAGCGGCAGTCGGGGGAGCGCCAGC	20488
Db	18597	CGTTTGCCCGCCACTGGGGGAGACGTTAAATTCAGCGGCAGTCGGGGGAGCGCCAGC	18656
Qy	20489	GTAGGGCTGGGGCGCCCAACAGCAGGTAAACAAACAGACAGACAGAGGAATGTAGC	20548
Db	18657	GTAGGGCTGGGGCGCCCAACAGCAGGTAAACAAACAGACAGACAGAGGAATGTAGC	18716
Qy	20549	GGTTAAATTAATCTGCTTACAAATCGCGGGCGCGCGCGGTCAACGCCAGGTCCATTAAAA	20608
Db	18717	GGTTAAATTAATCTGCTTACAAATCGCGGGCGCGCGCGGTCAACGCCAGGTCCATTAAAA	18776
Qy	20609	CACACGGCGCCCAACCCCAACAGGGGGGGCGGGCCCTGGAAACGGCGTTCTTCCAAATCG	20668
Db	18777	CACACGGCGCCCAACCCCAACAGGGGGGGCGGGCCCTGGAAACGGCGTTCTTCCAAATCG	18836
Qy	20669	CAAGAACCGCGTCACAAAAAGGGCTGTGTTTAAACCAATTTTGTGCCATCGGGTTTCGT	20728
Db	18837	CAAGAACCGCGTCACAAAAAGGGCTGTGTTTAAACCAATTTTGTGCCATCGGGTTTCGT	18896
Qy	20729	TTTCAGATACGGAAACGGCTGCTCCAAAAACACCCAAACGGGGGTGTCTCAACGGCCAT	20788
Db	18897	TTTCAGATACGGAAACGGCTGCTCCAAAAACACCCAAACGGGGGTGTCTCAACGGCCAT	18956
Qy	20789	CTCATCTCTATGTGGGGATGGGGGTGTAGCCCTGAGACTCAGATCCGGCGGGGTAA	20848
Db	18957	CTCATCTCTATGTGGGGATGGGGGTGTAGCCCTGAGACTCAGATCCGGCGGGGTAA	19016
Qy	20849	GTCTCCAGACGGCGCCACCTTTCTCAAAATCTTCACGCCGGAACGACGGCGGTCT	20908
Db	19017	GTCTCCAGACGGCGCCACCTTTCTCAAAATCTTCACGCCGGAACGACGGCGGTCT	19076
Qy	20909	CCGACGCTGAAGCAGCAGGGGGATCTACAGTGTGTGTTAAACGTGGGGCTACCCAAAGT	20968
Db	19077	CCGACGCTGAAGCAGCAGGGGGATCTACAGTGTGTGTTAAACGTGGGGCTACCCAAAGT	19136
Qy	20969	GTGCACAAGTCTCCCGGGGTACAGGCCCGTAGCGTACAGTACAGTACAGAGGGC	21028
Db	19137	GTGCACAAGTCTCCCGGGGTACAGGCCCGTAGCGTACAGTACAGTACAGAGGGC	19196
Qy	21029	GTAGCTGGCGATGTTAAACGGGACCCCGAGGCCATGTGGGGGACCTGTGTCACACTG	21088
Db	19197	GTAGCTGGCGATGTTAAACGGGACCCCGAGGCCATGTGGGGGACCTGTGTCACACTG	19256
Qy	21089	GCAGGACAGCTCCCCCGGACGACAGTAAACCTACACAACAAACGTGACAGAGGGAGAC	21148
Db	19257	GCAGGACAGCTCCCCCGGACGACAGTAAACCTACACAACAAACGTGACAGAGGGAGAC	19316
Qy	21149	CATCCGCGCAGGTCCCGGGGGTTCACCGGCACATTAACGATGCGCCGATCTGTGGGGCG	21208
Db	19317	CATCCGCGCAGGTCCCGGGGGTTCACCGGCACATTAACGATGCGCCGATCTGTGGGGCG	19376
Qy	21209	CCTGTAAATTAAGATCCACACAGTAAAGCAGCTGTGTACCCCTGTGACCTGTGTAGTGGC	21268
Db	19377	CCTGTAAATTAAGATCCACACAGTAAAGCAGCTGTGTACCCCTGTGACCTGTGTAGTGGC	19436
Qy	21269	GTCGGGCCCTGTATACCGCCCAAAATTTCTCACTGTGAACCCCTACACGGGCCGAG	21328
Db	19437	GTCGGGCCCTGTATACCGCCCAAAATTTCTCACTGTGAACCCCTACACGGGCCGAG	19496
Qy	21329	ATCGCCCTCGCGCGGTCCCGGAAGCCCTGCGCCGCAAAAGGGCGGGGA	21379
Db	19497	ATCGCCCTCGCGCGGTCCCGGAAGCCCTGCGCCGCAAAAGGGCGGGGA	19547

RESULT 3
AF029302
LOCUS
DEFINITION
10595 bp DNA linear VRL 21-NOV-1997
Rhesus monkey rhadinovirus H26-95 glycoprotein B, DNA polymerase,
and interleukin-6 homolog genes, complete cds; and thymidylate
synthase homolog gene, partial cds.
AF029302.1 GI:2625041
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Rhesus monkey rhadinovirus H26-95
Rhesus monkey rhadinovirus H26-95
viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
REFERENCE
AUTHORS
1 (bases 1 to 10595)
Destosiatis, R.C., Sasseville, V.G., Czajak, S.C., Zhang, X.,
Manfield, K.G., Kaur, A., Johnson, R.P., Lackner, A.A. and Jung, J.U.
TITLE
A herpesvirus of rhesus monkeys related to the human Kaposi's
sarcoma-associated herpesvirus
J. VIROL. 71 (12), 9764-9769 (1997)
JOURNAL
MEDLINE
PUBMED
98037693
9371642
2 (bases 1 to 10595)
Destosiatis, R.C., Sasseville, V.G., Czajak, S.C., Zhang, X.,
Manfield, K.G., Kaur, A., Johnson, R.P., Lackner, A.A. and Jung, J.U.
TITLE
Direct Submission
Submitted (08-OCT-1997) Microbiology, New England Regional Primate
Research Center, 1 Pine Hill Drive, Southborough, MA 01772-9102,
USA
FEATURES
source
1. 10595
/organism="Rhesus monkey rhadinovirus H26-95"
/mol_type="genomic DNA"
/isolate="H26-95"
/db_xref="taxon:69256"
/note="related to Kaposi's sarcoma-associated herpesvirus
(KSHV or human herpesvirus-8)."
<1. 498
/note="ORF 7"
/codon_start=1
/product="unknown protein"
/protein_id="AAC58685.1"
/db_xref="GI:2625042"
/translation="ORFGLITGRLTQSDLPFRANVVAACFEAGMLPHKMLVSE
MIPQIQPKMDIDQTRNRYQDPEDLNVAQSAFCFIRELVSAVLRNMTKTLRI
FSLAREKLISLNDVAGLTSGLYTEDAPLVLSQNGWIFKDLALYHHLQSD
GHDDN"
485..2974
/note="ORF 8: similar to human herpesvirus-8 (HHV-8)
glycoprotein B"
/codon_start=1
/product="glycoprotein B"
/protein_id="AAC58686.1"
/db_xref="GI:2625043"
/translation="MNTNTRRLRAMVVIATIGVANGENTTPKATTTAKTPGP
STTPPENPRAEAFKFRYCSASATGELFRFNLEKTCPTGDEKTHOEGILMTKRYV
PHIFKRYKRYATSVTVRGMTETAVTGKOEIRVPOIETINMDITTCOSSKRVN
VNGIVNTYDRDTNQTFLQPEVLTDNIQRFQSPVLYTTPGPGIYRVNTVNC
EIVDMARSAEPEYFEVTAIGDIVEVSPCHNDSCVAEKTENGAGAVLNVTYV
FAPATTEETRVADSGEYVSWKADPKSAVCAVLMKTFPRAIQTDEASATYV
DYATFTSPLSEVANTGTGYSCLDEVIQKTDITIKLSDTHYTNCSAQYTEGGLF
LLMQPLTSLIVDEMGLNGTTPAPRATTSYRSRVNTNQAIDNLAAPLOLQAY
DKURASINKVLELSRAKREOVRODTYMYELSKINPISVMTAIGRPVSAFVGAI
SVYDCAVDAQASVSIKSLRSTPGMCYSRPVTFERLNTLFGOLPDRNEIILT
NOVEACKETCEHYFIASNTYYKDYVFKKINTSEISLGFIALNLSFIEINDRYV
IEYLSAEKKEISGSVDIETMPREYNYTORLAGLEDONTIDLNRDLARLSEIV
ADLQGRTVVAVASVITLFGSISVGFNFKSPRGMLMILYIVAYVLYFALRR
TNAIAQPIRMATYPIDDKMPGSGKIDQCIKNTILAGHMLQDOEERRRLDEOQRAPS
LFRASDGLKRRFRGKPLENEADEYEMSK"
CDS
/note="ORF 9: similar to human herpesvirus-8 (HHV-8) DNA
polymerase"
/codon_start=1
/product="DNA polymerase"

/protein_id="AAC58687.1"
/translation="MDEFNPLYGRGPRPHSHRGTDAPAPAGAAVOPPEVCRLIPA
CIRTPAGGAMIPVTIPEPPYFENGARGLVLANESMTARBARKVAPDPOQSTFE
HADVYETTYAADRCAEVRSPROTDLIIPGDTLIGRDEDSVGVNVPPOOYFVA
KVPAGINVTHTLDOALKNTGRACGFSRTRVVKRLTKTYDAEHYETETSSGSM
STLSDRLVACGCEVESNDVAFVLDHGTTEGWSACARATPAAADARLALFED
CSMEDLSVADRSDMPRYRIVADIECTGAGPCATRODAVIOISCVETTRBEAP
NPNILFVSOTCDPDTDLVEPSEEDMLVSEFAMI RDEYDFLGVNINSFIDL
ITRASOVYNLRLNEYRKIKGSIIEVEHPGGGGGMRYSKIKIGIYVIDMYOYCR
EKLSIDYKIDYVACROICGKEDVSKDIPPLFRSGGGRARVSGVCWDSYVMDL
LKRMTHIVEISELAKLAKTOARRVYLDGQOLRYFSCLEBAARENTILVPPTEGCG
YOGATVINLPFGYDEPVLVVDASLTPSTIQANHCYSTHMGRLDHLHPNTPDY
EIFVLGSEVHYEKKARBSLRLRLTWLEKRAIRTLAACDDSLTILDKOOLA
IKVTCNAVYGTGTVASGLPLPCINIAETVTLRGRTMLMSKSYEALATTEDTLRLRE
VTRAHGRRVYVGGDSDLEIADGSAEVAFCGLDARIADLEPPRIKAEAKT
FKCLILTKRYATIGLNDKMWKGVLDLRTKCKRQVOEGRALIDLVILADPVRKA
RLCKRPHAVYEEGIPAGFIKIVEYLNASYDLNRNVPFIEULTSTELSRVCOYK
TNLPHLAVYOKLASCEELPOVHDRIYFVDAVAPSLSDLSLAEHPDYVRKHOIPVAV
DLVFDKLVHGAANIQLCGNNADTVAILYNPLNPKYLS"
6231..7481
/note="ORF 10"
/codon_start=1
/product="unknown protein"
/protein_id="AAC58688.1"
/db_xref="GI:2625045"
/translation="MLVNELSVYLDGMEVTFHNGREFSVNLRLQTEKFGHGYARVL
PFLDOLHOFAGLVTRLELPFSDCAVALIAPLDGADAAVARAGVFLDSSRP
LTVWNASGHRITRFLFLFKPDLERAVTYVGGGAGRSSETPKTCSTELSGP
LRYSGASOTSPPSPVAPPTASVACISLRLQVDFSDAHRARAPKRVFSN
SGGNVCKASVHTLSRCKTAQKEITTYARDPNAELVYVAPGCVYLPHTHGRGLGYA
DAKRTIOPSSAEVROLIFQOGAARGADIAVTVAPPELVYVLPALLSCCTHL
FLFNPNGTPTTIKRDPLVAAAPCPVRLSSADAPDRDLVAPDGTALSTNAETIPVG
FPGVVAECHVTSRDNGVHERMNH"
7490..8719
/note="ORF 11"
/codon_start=1
/product="unknown protein"
/protein_id="AAC58689.1"
/db_xref="GI:2625046"
/translation="MGPVAFRFGEMQTSLVNDNGPRYSLSLWANTIHGTYLTVNR
SELCTEERSGCLPACPSIGRLVGRFGAPASATIGDGTGRTVFAFGRRDPLIV
PAYVERADRELYRVAPOTTRRSRGIAFVAVYVPRPGFLPRDPRVIALTD
ACQESGRSLSEBWKIKGFPLSDETHAPFLTKTQPTFKRCKRLIMDDQSA
VNTVYLGKHQVAVTVRPETIYTDGPVATLSLTNAPLAFHNPYFELPMSTTAL
FPPVYVGLTVCIPPCNSKFRVRYVAFNFKLTAIISNHNAGGFRIOCEMPN
REIELVTNVSQAPVYISTGTQGAIFVAFRFGAPAKRLQLGHRSRALDELPGVT
VDSOKLCRFETWYLFST"
complement(8891..9514)
/note="ORF K2: similar to human herpesvirus-8 (HHV-8)
interleukin-6"
/codon_start=1
/product="interleukin-6 homolog"
/protein_id="AAC58690.1"
/db_xref="GI:2625047"
/translation="MPPVWVLYFLSCMAASPLAPPPAAGINVLDPQANRASIDR
TKRRLSEVGINLQRMVYLCHNSTLRLVREYVIMSEVTFPIIMSVEQORREFRAE
CNMAARGLRAYSYLTRLMLDLPAGDADAALISAVTFLYSALDSILEEPVANNK
IGCAEENETVRALGSGSPRDYVLSAFRILEYLQMLRDRRAIAM"
complete(9747..>10595)
/note="ORF 70: similar to human herpesvirus-8 (HHV-8)
thymidylate synthase"
/codon_start=1
/product="thymidylate synthase homolog"
/protein_id="AAC58691.1"
/db_xref="GI:2625048"
/translation="OTLAHDLIRIKGCVREDRTGVTGSVEQLARVNLUREDFLLT
TKRVFRGAVVEELLMFIRGSTDSLELRGVAKIWDHGSRAFLAAGCFDRREGDLP
VVGQWRHFGAERGADANYEGGVQDLVYVVDLIRPHDRITVCAANNPADLAFMA
LPPCHVLCQFYVARGELSCOLYQRSADMKDGVFNATSYALLTYLILAHYGLTPGGFV
HETLGAHVVNNHVDPLLDLRRTPRFPRLIKRKYARLEDFRADLSLEGDPHBI
EMEMAY"

BASE COUNT

2307 a 3372 c 2971 g 1945 t

ORIGIN

Query Match 19.9%; Score 7957; DB 1; Length 10595;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 8257; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 13117 TGTACTGCGCCCCCGGTACGTTGAGTTTCTCAACAGACACCAGCTGTTCAAGGGC 13176
|||||
DB TGTACTGCGCCCCCGGTACGTTGAGTTTCTCAACAGACACCAGCTGTTCAAGGGC 2146
OY 13177 CAGCTGGGACCCAGAAAGAAATCATCTGACGGACAACAGGTGGAGCGTGCAGAG 13236
|||||
DB CAGCTGGGACCCAGAAAGAAATCATCTGACGGACAACAGGTGGAGCGTGCAGAG 2206
OY 13237 ACGTGGCAACTACTTATAGCGAGCAACGTAACCTACTACTCAAAAGACTAGCTTC 13296
|||||
DB ACGTGGCAACTACTTATAGCGAGCAACGTAACCTACTACTCAAAAGACTAGCTTC 2266
OY 13297 GTGAAAAAATTAACACCTCGAGATATCACCCGTGAGTTGATGCGCCGTGAACCTG 13356
|||||
DB GTGAAAAAATTAACACCTCGAGATATCACCCGTGAGTTGATGCGCCGTGAACCTG 2326
OY 13357 TCGTTTATAGAAATATGATTTCAAGGTCAATCGAGCTGTACAGCCGCGGAGAAAAAG 13416
|||||
DB TCGTTTATAGAAATATGATTTCAAGGTCAATCGAGCTGTACAGCCGCGGAGAAAAAG 2386
OY 13417 CTGTCCGGGAGCGTTTGTGATATGAAACGATGTTCAAGGAATACAACTACTAGACGCA 13476
|||||
DB CTGTCCGGGAGCGTTTGTGATATGAAACGATGTTCAAGGAATACAACTACTAGACGCA 2446
OY 13477 CGCCTGGCGGAGCTCCGGGAGAGCTGGACAACAGATGACCTGAACCGGACCGCCTG 13536
|||||
DB CGCCTGGCGGAGCTCCGGGAGAGCTGGACAACAGATGACCTGAACCGGACCGCCTG 2506
OY 13537 GCCCGGACCTGTCCGAAATAGTGGCGGACCTGGGCGCATGTGCGCGCGGACGCTGTAAC 13596
|||||
DB GCCCGGACCTGTCCGAAATAGTGGCGGACCTGGGCGCATGTGCGCGCGGACGCTGTAAC 2566
OY 13597 GTGGCAGATAGCGATATTAACCTGTTCGATCAATCGTAGCGGGTTCATTAACTTTTA 13656
|||||
DB GTGGCAGATAGCGATATTAACCTGTTCGATCAATCGTAGCGGGTTCATTAACTTTTA 2626
OY 13657 AAGAGTCCGTTGCGGGGCGATGCTCATGATCTGTGATTTGGCGGCTGCTGATGCTG 13716
|||||
DB AAGAGTCCGTTGCGGGGCGATGCTCATGATCTGTGATTTGGCGGCTGCTGATGCTG 2686
OY 13717 TTTGCGCTAAACCGGCGGACCAAGGCCATCGGCCCGCCCATATGAGATGATACCCC 13776
|||||
DB TTTGCGCTAAACCGGCGGACCAAGGCCATCGGCCCGCCCATATGAGATGATACCCC 2746
OY 13777 GACATAGACAAATATGACACCTCTGGCGGTAAAGTCGACAGAGACAGATTTAAAAAATT 13836
|||||
DB GACATAGACAAATATGACACCTCTGGCGGTAAAGTCGACAGAGACAGATTTAAAAAATT 2806
OY 13837 CTCGCCGCGATGCAACGCTACAGAGAGAGAGCGTAGCGGTTAGAGAAACAGCAGAG 13896
|||||
DB CTCGCCGCGATGCAACGCTACAGAGAGAGAGCGTAGCGGTTAGAGAAACAGCAGAG 2866
OY 2807 CTCGCCGCGATGCAACGCTACAGAGAGAGAGCGTAGCGGTTAGAGAAACAGCAGAG 2866
|||||
DB CTCGCCGCGATGCAACGCTACAGAGAGAGAGCGTAGCGGTTAGAGAAACAGCAGAG 2866
OY 13897 TCAGCGCCCTGCGCTTTTCCGGCGGCGGTCAAGCGAGCTAAAAACGTCGTTTAGGGGAAT 13956
|||||
DB TCAGCGCCCTGCGCTTTTCCGGCGGCGGTCAAGCGAGCTAAAAACGTCGTTTAGGGGAAT 2926
OY 13957 AAACCGCTGGAAGAGAGAGCTCAAGATATGAAATGAGCAATTAACACACCCACAC 14016
|||||
DB AAACCGCTGGAAGAGAGAGCTCAAGATATGAAATGAGCAATTAACACACCCACAC 2986
OY 14017 GCCTGTACTTCCGCGCGCGAGAGCGCGGCGCAATGATTCGCGCAACCGCGGCTGC 14076
|||||
DB GCCTGTACTTCCGCGCGCGAGAGCGCGGCGCAATGATTCGCGCAACCGCGGCTGC 3046
OY 14077 CCGAGACGCTTAGGCGCGCGGCGGCTGCTGTATCAATATGATTTCTTTAAC 14136
|||||
DB CCGAGACGCTTAGGCGCGCGGCGGCTGCTGTATCAATATGATTTCTTTAAC 3106

OY 14137 CCGTACTGGGCGCTCGCGGACACGCCCCCACTCACAGAGGACCGATGCTCCGCC 14196
|||||
DB CCGTACTGGGCGCTCGCGGACACGCCCCCACTCACAGAGGACCGATGCTCCGCC 3166
OY 14197 CCTGCCGCGCGGACCGCTTACAGCGCGCACAGAGCTTTTGAAGCTCATCCCGCTGC 14256
|||||
DB CCTGCCGCGCGGACCGCTTACAGCGCGCACAGAGCTTTTGAAGCTCATCCCGCTGC 3226
OY 14257 CTCGGAACGCGGAGGCGGAGGATGATCCCGGACAGATCCGTTCCCGCAACGTTAC 14316
|||||
DB CTCGGAACGCGGAGGCGGAGGATGATCCCGGACAGATCCGTTCCCGCAACGTTAC 3286
OY 14317 TTTGGAACGCTGCTCGCGGAGAGCTGTGCTCCGCAAGAACGGTTCATGAGCGCG 14376
|||||
DB TTTGGAACGCTGCTCGCGGAGAGCTGTGCTCCGCAAGAACGGTTCATGAGCGCG 3346
OY 14377 CGGACCGCAAGCCCGTGCGCCGAGACCCCAAGACAAATCCATCAGCTTTACGCGTAC 14436
|||||
DB CGGACCGCAAGCCCGTGCGCCGAGACCCCAAGACAAATCCATCAGCTTTACGCGTAC 3406
OY 14437 GACGTCGTTGAACAACTAGCGCGCGGACAGGTGTGCGGAGTACTTACGCGCTTCAA 14496
|||||
DB GACGTCGTTGAACAACTAGCGCGCGGACAGGTGTGCGGAGTACTTACGCGCTTCAA 3466
OY 14497 ACGGACATTTATCCCAAGCGGAAACGCTGCTCAAGCTCTGCGGCGCAACCGAGACGCAAC 14556
|||||
DB ACGGACATTTATCCCAAGCGGAAACGCTGCTCAAGCTCTGCGGCGCAACCGAGACGCAAC 3526
OY 14557 AGCGTGTGCTGAACGCTGCTCCGTCACAGAGTATATTTCTACGCGAAGCTTCAAGCGGC 14616
|||||
DB AGCGTGTGCTGAACGCTGCTCCGTCACAGAGTATATTTCTACGCGAAGCTTCAAGCGGC 3586
OY 14617 ATTAACTGACCCCAATCTCTCCAGAGCCCTCAAGAAACACAGCGCGCTGCGCCGTC 14676
|||||
DB ATTAACTGACCCCAATCTCTCCAGAGCCCTCAAGAAACACAGCGCGCTGCGCCGTC 3646
OY 14677 GCGTTCGAGCAGAGAGTGAACAAAGAAATTTCAAAAGGTACAGAGCTGCGGAGCAT 14736
|||||
DB GCGTTCGAGCAGAGAGTGAACAAAGAAATTTCAAAAGGTACAGAGCTGCGGAGCAT 3706
OY 14737 CCGGTCACGGAATACGCTATGCTCGCGGTTCCATGCTCTGACACCTCAAGCACCGCTC 14796
|||||
DB CCGGTCACGGAATACGCTATGCTCGCGGTTCCATGCTCTGACACCTCAAGCACCGCTC 3766
OY 14797 GTGCGGTGCGGAGTGTGAGTGTGAGTCAAAACGAGCGCGCTGCGCGGTTGCTGTG 14856
|||||
DB GTGCGGTGCGGAGTGTGAGTGTGAGTCAAAACGAGCGCGCTGCGCGGTTGCTGTG 3826
OY 14857 GATCACGGGTTTACACGTTGCGGTGTACTGTGTCGCGCGCGCACCGCCCGCTGCGC 14916
|||||
DB GATCACGGGTTTACACGTTGCGGTGTACTGTGTCGCGCGCGCACCGCCCGCTGCGC 3886
OY 14917 GCCAGAGTGTCCAGAGCGCCCTGAGATTGACGCTGACAGCTGGAGAGACCTCAGCTTCAA 14976
|||||
DB GCCAGAGTGTCCAGAGCGCCCTGAGATTGACGCTGACAGCTGGAGAGACCTCAGCTTCAA 3946
OY 14977 GCGAGCGGACGAGACTGCGCCCGGTAACCGGATCGGCGCTTGAATGAGAGCACTGGA 15036
|||||
DB GCGAGCGGACGAGACTGCGCCCGGTAACCGGATCGGCGCTTGAATGAGAGCACTGGA 4006
OY 15037 GAGCGGAGATTTCCTGCGCACAGCGGCGGAGCGGCGGTATCCAGATCTCCGCTGC 15096
|||||
DB GAGCGGAGATTTCCTGCGCACAGCGGCGGAGCGGCGGTATCCAGATCTCCGCTGC 4066
OY 15097 TTTTACAGACGAGGAGGAGCGCGCCCAATCCGCAAACTATCTTACAGCTGCGGAGC 15156
|||||
DB TTTTACAGACGAGGAGGAGCGCGCGCCCAATCCGCAAACTATCTTACAGCTGCGGAGC 4126
OY 15157 TGGGACGCTATCCGAGACGAGAGCTTTTGGAGTTTCCGTGGGAATATGACATGCTGGTG 15216
|||||
DB TGGGACGCTATCCGAGACGAGAGCTTTTGGAGTTTCCGTGGGAATATGACATGCTGGTG 4186

QY 15217 TCGTCTTCGCCATGATCCGCACTTCGAGGTGAGACTTTTAAACCGGCTATACATCTCA 15276
Db 4187 TCGTCTTCGCCATGATCCGCACTTCGAGGTGAGACTTTTAAACCGGCTATACATCTCA 4246
QY 15277 AACTTGATCTCCCGTACCTAATACGCGAGCGTCCAGGTGATACAACCTTCGATTAAAC 15336
Db 4247 AACTTGATCTCCCGTACCTAATACGCGAGCGTCCAGGTGATACAACCTTCGATTAAAC 4306
QY 15337 GAATACACAAAAATAAAAAACCGGCTCCATCTTTGAAGTTTCACGAGCCCGTGGCGGGGA 15396
Db 4307 GAATACACAAAAATAAAAAACCGGCTCCATCTTTGAAGTTTCACGAGCCCGTGGCGGGGA 4366
QY 15397 GGGGGGTTGATGAGTCGCTGCTCAAAAAATTAATAGCGGGGATTCGTCCCATAGACATG 15456
Db 4367 GGGGGGTTGATGAGTCGCTGCTCAAAAAATTAATAGCGGGGATTCGTCCCATAGACATG 4426
QY 15457 TACACAGGTGTCGCGCAAAAAGCTCAGCTCTCCGACTACAAACTGGACAGGTGGCGAG 15516
Db 4427 TACACAGGTGTCGCGCAAAAAGCTCAGCTCTCCGACTACAAACTGGACAGGTGGCGAG 4486
QY 15517 CAGTGTCTGGGTGGAAAAAAGAGAGCATCTGTACAGAGACATCCCTCTGTTTCCG 15576
Db 4487 CAGTGTCTGGGTGGAAAAAAGAGAGCATCTGTACAGAGACATCCCTCTGTTTCCG 4546
QY 15577 TCAGGTCCGGGCGGCGAGGCTAAGTGGGCGAGCTATTGGTGAATGAGACTGGTCTGGTG 15636
Db 4547 TCAGGTCCGGGCGGCGAGGCTAAGTGGGCGAGCTATTGGTGAATGAGACTGGTCTGGTG 4606
QY 15637 ATGACCTCTTAAAAATGTTTATGATACAGTGAATTCGAGATTTAGCAAGCTGACC 15696
Db 4607 ATGACCTCTTAAAAATGTTTATGATACAGTGAATTTGGAGATTTAGCAAGCTGACC 4666
QY 15697 AAGATTCAAGGCCAGGCGCTCTGACGAGAGGCCAAGCTCCGCTGTTCTCTGCTG 15756
Db 4667 AAGATTCAAGGCCAGGCGCTCTGACGAGAGGCCAAGCTCCGCTGTTCTCTGCTG 4726
QY 15757 CTGGAGGCGGCGGCGAGGGAACCTTATCTCCGCTTCCACGCGCCGAGGAGACAGGG 15816
Db 4727 CTGGAGGCGGCGGCGAGGGAACCTTATCTCCGCTTCCACGCGCCGAGGAGACAGGG 4786
QY 15817 GGCCTATCAGGCGCGAGGCTGATCAACCCCATTCGGGGTTTTACGACGAGCGGTCTG 15876
Db 4787 GGCCTATCAGGCGCGAGGCTGATCAACCCCATTCGGGGTTTTACGACGAGCGGTCTG 4846
QY 15877 GTGCTGATTTTTCAGCCTGTATACCGAGCATCATCAGGCGGACCAACCTGTGCTACTCC 15936
Db 4847 GTGCTGATTTTTCAGCCTGTATACCGAGCATCATCAGGCGGACCAACCTGTGCTACTCC 4906
QY 15937 ACCATGATACAGGAGAGAACCTCGACCTGACACCCCAACCTGACGCGCGGAGCATACGAG 15996
Db 4907 ACCATGATACAGGAGAGAACCTCGACCTGACACCCCAACCTGACGCGCGGAGCATACGAG 4966
QY 15997 ACGTTCGTGCTAGGCGGCGAGCGGATATTTTGTAAAAAACAACAAGGCGGAGTCTG 16056
Db 4967 ACGTTCGTGCTAGGCGGCGAGCGGATATTTTGTAAAAAACAACAAGGCGGAGTCTG 5026
QY 16057 CTGGGAAGACTCTAAACCTGTGTGTTAGAAAAAGCGAAGGCGATCCGCGGCG 16116
Db 5027 CTGGGAAGACTCTAAACCTGTGTGTTAGAAAAAGCGAAGGCGATCCGCGGCG 5086
QY 16117 GGGTGGAGTACCCCGCTGCTAAAAACCATTTAGATTAACAACACAGTGGCCATCAAGGTG 16176
Db 5087 GGGTGGAGTACCCCGCTGCTAAAAACCATTTAGATTAACAACACAGTGGCCATCAAGGTG 5146
QY 16177 ACATGTAAAGCGGTTTACGGGTTACCGGGGTGAGCGGCGCTCTCCCATGCAATTAAC 16236
Db 5147 ACATGTAAAGCGGTTTACGGGTTACCGGGGTGAGCGGCGCTCTCCCATGCAATTAAC 5206
QY 16237 ATAGCGGAAACCGTGAAGCTTCGCGGGGCGCACGATGCTGAGATGTCAAAAGTCTTAAC 16296
Db 5207 ATAGCGGAAACCGTGAAGCTTCGCGGGGCGCACGATGCTGAGATGTCAAAAGTCTTAAC 5266
QY 16297 GAGGCGCTGACGAGAGAACTCGGAGACGCTCTCGGTGCGAGGTGACCGCCGCTCAC 16356

Db 5267 GAGGCGCTGACGAGAGAACTCGGAAACCGCTCTGCTGCGAGGTGACCGCCGCTCAC 5326
QY 16357 GCGCGCGGTTTTCGCGTGTCTACAGGTGACACGACGCTCCCTTTATACGGTCTGACG 16416
Db 5327 GCGCGCGGTTTTCGCGTGTCTACAGGTGACACGACGCTCCCTTTATACGGTCTGACG 5386
QY 16417 TATTCCGCGAAGCCGTTTCCGCTTCTGTGACGATCTGGCCGACAGATCACTGCGGAC 16476
Db 5387 TATTCCGCGAAGCCGTTTCCGCTTCTGTGACGATCTGGCCGACAGATCACTGCGGAC 5446
QY 16477 CTGTCCCGCCACCCATTAAAGCTAAGAGGCGGAAAGAGCTTCAAGTGTCTGTCTG 16536
Db 5447 CTGTCCCGCCACCCATTAAAGCTAAGAGGCGGAAAGAGCTTCAAGTGTCTGTCTG 5506
QY 16537 ACGAAAAAGGCTTACATCGGGGCTCTAATTGAACAGCAAAATGCTCATGAAGGGGTGAC 16596
Db 5507 ACGAAAAAGGCTTACATCGGGGCTCTAATTGAACAGCAAAATGCTCATGAAGGGGTGAC 5566
QY 16597 CTCATTGCAAAAAGGCTGTGCAAGTTTGTCCAGAGCGATGCCGCCATCTGTGACCTG 16656
Db 5567 CTCATTGCAAAAAGGCTGTGCAAGTTTGTCCAGAGCGATGCCGCCATCTGTGACCTG 5626
QY 16657 GTGCTCCAGATCCGAGAGTCAAGGCTCGCGGGCGGCTGTTGTGCAAGCGCGCGGAC 16716
Db 5627 GTGCTCCAGATCCGAGAGTCAAGGCTCGCGGGCGGCTGTTGTGCAAGCGCGCGGAC 5686
QY 16717 GCGGTATACAGGAGGAGGCTGCCGCTGCTTATTAATAATCTATAGAGTCTCAACGCG 16776
Db 5687 GCGGTATACAGGAGGAGGCTGCCGCTGCTTATTAATAATCTATAGAGTCTCAACGCG 5746
QY 16777 AGCTATCTGAGCTCCGAAACAGCGTGTGCCATCGAGCATGTTAACTTCCACCGAG 16836
Db 5747 AGCTATCTGAGCTCCGAAACAGCGTGTGCCATCGAGCATGTTAACTTCCACCGAG 5806
QY 16837 CTCAGCGCGCGCTGTGCGATTCAGACCAACCACTGCCACCTGGGGGTATCCAA 16896
Db 5807 CTCAGCGCGCGCTGTGCGATTCAGACCAACCACTGCCACCTGGGGGTATCCAA 16956
QY 16897 AAGCTGGGAGAGAGTGTGCGAGAGTCCCGACAGTCAAGATGAAATCCCTACGTGTT 16956
Db 5867 AAGCTGGGAGAGAGTGTGCGAGAGTCCCGACAGTCAAGATGAAATCCCTACGTGTT 5926
QY 16957 GTTGACGCGCGCGGCTCCCTAAAGTGTGAGCTGTGCCGAACCCGGAATTAAGTCAACAG 17016
Db 5927 GTTGACGCGCGCGGCTCCCTAAAGTGTGAGCTGTGCCGAACCCGGAATTAAGTCAACAG 5986
QY 17017 CACCAATTCGCGTGGCGGTGCGACCTAATTTGCAAACTGCTGACGCGCGGCGCAC 17076
Db 5987 CACCAATTCGCGTGGCGGTGCGACCTAATTTGCAAACTGCTGACGCGCGGCGCAC 6046
QY 17077 ATCTTCAGTGTCTGTTCGGCAACAACGCGGAGACACGAGTGGCCATCTCTCAATTTT 17136
Db 6047 ATCTTCAGTGTCTGTTCGGCAACAACGCGGAGACACGAGTGGCCATCTCTCAATTTT 6106
QY 17137 CTCACGTCCTCGTATTAAGCTGTTCTGTGACGCCAATTGGAGACGCCAACAATAAGAG 17196
Db 6107 CTCACGTCCTCGTATTAAGCTGTTCTGTGACGCCAATTGGAGAGGCCAACAATAAGAG 6166
QY 17197 CCGCGGACGAGAGTCCGAGGAGAGCTGAGCGGCGGAGGCGGCAACGAGAGCCG 17256
Db 6167 CCGCGGACGAGAGTCCGAGGAGAGCTGAGCGGCGGAGGCGGCAACGAGAGCCG 6226
QY 17257 CACCATGCTGTGTTAAAGCACTGTGCTGCTCGCGGACTGGGAGGTACTTTTACCG 17316
Db 6227 CACCATGCTGTGTTAAAGCACTGTGCTGCTCGCGGACTGGGAGGTACTTTTACCG 6286
QY 17317 GGGTAGATTACGCTTCTCACTCAACCTGACCGGCTGCAACGTTCAAGGCGCACGCGGCTA 17376
Db 6287 GGGTAGATTACGCTTCTCACTCAACCTGACCGGCTGCAACGTTCAAGGCGCACGCGGCTA 6346
QY 17377 GCGCAGGCTCGACATCCCTTCTCGCTGACACAGTATCTCAACCAATTTTGGCGTGG 17436

Db 6347 CGCCAGGGTCCGACTCCCTTCTCGCTCGACAGTTACTCCACCACATTTTCGCTTCG 6406
QY 17437 ACTGATGACGGTCTCAAGAACTGCCCCCTTCCTCGACTGCGTGGCCCTTATGCGCC 17496
Db 6407 ACTGTGACGGCTCAAGAACTGCCCCCTTCTCGACTGCGTGGCCCTTATGCGCC 6466
QY 17497 GTTGGATTCCGCGCGACGCGGAGACGCGCGCTGAGCCCCCGGGTTCGTGCTGACTC 17556
Db 6467 GTTGGATTCCGCGCGACGCGGAGACGCGCGCTGAGCCCCCGGGTTCGTGCTGACTC 6526
QY 17557 CTCTCGCCCGCTGACCGTGTGGGTTAAACGCGAGGGCGGACACAGATCCGGTTCGCT 17616
Db 6527 CTCTCGCCCGCTGACCGTGTGGGTTAAACGCGAGGGCGGACACAGATCCGGTTCGCT 6586
QY 17617 CCTCTTCTAAAGCGGATCGACCTGGAGCGCGGCTGACGTACGCTTCGGCGAAGAGG 17676
Db 6587 CCTCTTCTAAAGCGGATCGACCTGGAGCGCGGCTGACGTACGCTTCGGCGAAGAGG 6646
QY 17677 CGGCGCGGCTCGGAGGGACACCCCAAGCCACCTGCGCGACCGAAGCCTGCGCGTGG 17736
Db 6647 CGGCGCGGCTCGGAGGGACACCCCAAGCCACCTGCGCGAGACCGAAGCCTGCGCGTGG 6706
QY 17737 ACCCTGCGGCTCTCGCGCGAGGGCTCTCAGACGTGCCCCATTCCTTCTGTTGCGTATT 17796
Db 6707 ACCCTGCGGCTCTCGCGCGAGGGCTCTCAGACGTGCCCCATTCCTTCTGTTGCGTATT 6766
QY 17797 TCCACGGGCAACTGGTGGGCTGCTAAGCCTGTTGGGTTACAGGTGAGGCGGTTTTC 17856
Db 6767 TCCACGGGCAACTGGTGGGCTGCTAAGCCTGTTGGGTTACAGGTGAGGCGGTTTTC 6826
QY 17857 GGATGACGCGGCGCACAGGAGCGCGGATCTCCCGCAAAATACGTACAGTTAGTAACTC 17916
Db 6827 GGATGACGCGGCGCACAGGAGCGCGGATCTCCCGCAAAATACGTACAGTTAGTAACTC 6886
QY 17917 CGGCGGTAAGCTCTGCAAGGGGCTCGTTCACACGCTGCCGCTGGCGGTGTAAGAGGCG 17976
Db 6887 CGGCGGTAAGCTCTGCAAGGGGCTCGTTCACACGCTGCCGCTGGCGGTGTAAGAGGCG 6946
QY 17977 GCAAAATGAAATCATCTACGCTCCCGGGGACCCCAACCGCGATAGTCTGCGGCGACTC 18036
Db 6947 GCAAAATGAAATCATCTACGCTCCCGGGGACCCCAACCGCGATAGTCTGCGGCGACTC 7006
QY 18037 CGGACCGCTCTGCGCGACCCACACCGCGCGGCTGATTTGGGGGTCTACGCGCGACCGA 18096
Db 7007 CGGACCGCTCTGCGCGACCCACACCGCGCGGCTGATTTGGGGGTCTACGCGCGACCGA 7066
QY 18097 AAAAAACATCCACACTGGAAGCTCCGCGGAAGTCCGGGTTCAAGTTAACTTCCACAGG 18156
Db 7067 AAAAAACATCCACACTGGAAGCTCCGCGGAAGTCCGGGTTCAAGTTAACTTCCACAGG 7126
QY 18157 AGCGGCGCTGGGGGCGATCTGGGCTTCTGCTACGCGGCGTGGGACCGGAGCGCCCTATT 18216
Db 7127 AGCGGCGCTGGGGGCGATCTGGGCTTCTGCTACGCGGCGTGGGACCGGAGCGCCCTATT 7186
QY 18217 CGTGTCAACCCCGGCACTCTTGCTTCCGTTGCAACCAACCACTGCGCTATTCACACC 18276
Db 7187 CGTGTCAACCCCGGCACTCTTGCTTCCGTTGCAACCAACCACTGCGCTATTCACACC 7246
QY 18277 CAAGGTAACCCCGCAAGACTATTAAGAGACACCTTGTGGCGCGCGCGCGCTGCGC 18336
Db 7247 CAAGGTAACCCCGCAAGACTATTAAGAGAGACACCTTGTGGCGCGCGCGCGCTGCGC 7306
QY 18337 CGTGTGCGATTAACTCCGCGGAGACGCGCGCGGAGACCTGTCGCGTCCAGACAC 18396
Db 7307 CGTGTGCGATTAACTCCGCGGAGACGCGCGCGGAGACCTGTCGCGTCCAGACAC 7366
QY 18397 CGGCGCGCTCTTCATTAACGCGTTCACAATCCGCGTGTTCACAGGCGTGTCTCGGC 18456
Db 7367 CGGCGCGCTCTTCATTAACGCGTTCACAATCCGCGTGTTCACAGGCGTGTCTCGGC 7426
QY 18457 GGAGGTACAGTGTCCCTACGCGACAGGCGGTCTCAGCAAGCATGAACCATTTAGCGCA 18516
Db 7427 GGAGGTACAGTGTCCCTACGCGACAGGCGGTCTCAGCAAGCATGAACCATTTAGCGCA 7486

QY 18517 ACGATGGGAACACCGGTGCTGTTTCTTTCGCGGAGTGGACAGACTCGAGTCTAGTGGAC 18576
Db 7487 ACGATGGGAACACCGGTGCTGTTTCTTTCGCGGAGTGGACAGACTCGAGTCTAGTGGAC 7546
QY 18577 AAGGCGACGCGATACAGCTCCCTGCTGTGGCGCGCACATATTACAGAGGCTACCTG 18636
Db 7547 AAGGCGACGCGATACAGCTCCCTGCTGTGGCGCGCACATATTACAGAGGCTACCTG 7606
QY 18637 ACATGCTGAACAGTCAAGAGTGTGCTCAGCGAAGAGTCTCCGTGTCTGCGCGCATGC 18696
Db 7607 ACATGCTGAACAGTCAAGAGTGTGCTCAGCGAAGAGTCTCCGTGTCTGCGCGCATGC 7666
QY 18697 CCAGCATCGGAGAGCTGGTGGGAAAGGTTTCCCGGCTTGCCCTTTGCCAGCGCCACT 18756
Db 7667 CCAGCATCGGAGAGCTGGTGGGAAAGGTTTCCCGGCTTGCCCTTTGCCAGCGCCACT 7726
QY 18757 CTGGCGATCGGGGAACACGACCGTGTCTACGCGTTCCGCTACCGCGACACCCACTG 18816
Db 7727 CTGGCGATCGGGGAACACGACCGTGTCTACGCGTTCCGCTACCGCGACACCCACTG 7786
QY 18817 GACATAGTACCCCGCTGCTGAGCGCGCGGATGCGAGCTGTCTCGGGTTACGCT 18876
Db 7787 GACATAGTACCCCGCTGCTGAGCGCGCGGATGCGAGCTGTCTCGGGTTACGCT 7846
QY 18877 CCGCAACACGCGGGTGTGCGGATACGAGCTTAAGTATTGCGTGGCGATGTTACGGTG 18936
Db 7847 CCGCAACACGCGGGTGTGCGGATACGAGCTTAAGTATTGCGTGGCGATGTTACGGTG 7906
QY 18937 GTGCGCCCGCGGGGTCTCTACACTTTCCACAAGACCGGTTCCGATCGCGCTGACA 18996
Db 7907 GTGCGCCCGCGGGGTCTCTACACTTTCCACAAGACCGGTTCCGATCGCGCTGACA 7966
QY 18997 GACGCGTACCGAGGAGGCTCCAGGCTAACCTGTGAAGACCGTGTGAATAAATTCAA 19056
Db 7967 GACGCGTACCGAGGAGGCTCCAGGCTAACCTGTGAAGACCGTGTGAATAAATTCAA 8026
QY 19057 GGCCTTCCCGTCTTCTGAGAGAGACCGCACCATTTCTTAAACCAGAAACCAAG 19116
Db 8027 GGCCTTCCCGTCTTCTGAGAGAGACCGCACCATTTCTTAAACCAGAAACCAAG 8086
QY 19117 CCCTTTACCGAGCAAGATTTCGCGCTGATCATGACAACAGACGCGACGCGCTC 19176
Db 8087 CCCTTTACCGAGCAAGATTTCGCGCTGATCATGACAACAGACGCGACGCGCTC 8146
QY 19177 AACACCGTCTACCTGGAAGACGACGCTGAGAGGTGACCGTGACCCCGCCCGGAACA 19236
Db 8147 AACACCGTCTACCTGGAAGACGACGCTGAGAGGTGACCGTGACCCCGCCCGGAACA 8206
QY 19237 ATCGTACCGAGCGCGCGTGAACGCGGACCGCTGCTCACCGGTAAATGCGCAATCGCC 19296
Db 8207 ATCGTACCGAGCGCGCGTGAACGCGGACCGCTGCTCACCGGTAAATGCGCAATCGCC 8266
QY 19297 TTTGCGCAACCCATTAATTGAACTCCGTGTGCTGCACAAACGCGCATTTACGCGCC 19356
Db 8267 TTTGCGCAACCCATTAATTGAACTCCGTGTGCTGCACAAACGCGCATTTACGCGCC 8326
QY 19357 GTGGTGAAGTGGGCGCTACCGGTGACATCCACCCACTGTAAGAAATTTGTAAGTAC 19416
Db 8327 GTGGTGAAGTGGGCGCTACCGGTGACATCCACCCACTGTAAGAAATTTGTAAGTAC 8386
QY 19417 GGTAAACACTACGTTCCGCAATTAAACGCAAGTGAACGCGGATATTAGCAATACGCC 19476
Db 8387 GGTAAACACTACGTTCCGCAANTTAACGCAAGTGAACGCGGATATTAGCAATACGCC 8446
QY 19477 CACAACGCGGGTTCGGAATTCAGAGTGCAGAGTGCACGCAACCGGAGATTAAGATT 19536
Db 8447 CACAACGCGGGTTCGGAATTCAGAGTGCAGAGTGCACGCAACCGGAGATTAAGATT 8506
QY 19537 TTGTAACCAACGTTCCAGGCGCGCGGTATCATACACACCGGAGACGACGCTGGGGCA 19596
Db 8507 TTGTAACCAACGTTCCAGGCGCGCGGTATCATACACACCGGAGACGACGCTGGGGCA 8566

QY	19597	CCACATCTCGGTTCCGGCGCGGGTTCCGGCGCGGAGCAACCTCGGACGCTCCCGCC	195956
Db	8567	GCCATCTCGGTTCCGGCGCGGGTTCCGGCGCGGAGCAACCTCGGACGCTCCCGCC	8626
QY	19657	CACGATCGCGCGCCCTGGAGCTCGCGGGGGGGGTACAGTGGACAGCCAAACCTGTGT	19716
Db	8627	CACGATCGCGCGCCCTGGAGCTACCGGGGGGGGTACAGTGGACAGCCAAACCTGTGT	8686
QY	19717	AGGTTGAGACCATGTACCTGTTTCCAGGTAATTACTAATTAACCGTTTGTCTGTATC	19776
Db	8687	AGGTTGAGACCATGTACCTGTTTCCAGGTAATTACTAATTAACCGTTTGTCTGTATC	8746
QY	19777	GCTACACAAACGGCAACCGGTCTCATCTCGGGGGTCCGGCGCCCGGGAACACACAAG	19836
Db	8747	GCTACACAAACGGCAACCGGTCTCATCTCGGGGGTCCGGCGCCCGGGAACACACAAG	8806
QY	19837	GTCGCTCAAAACACCCCTTCCTCCGACCTTCGCACACAAACACAGTTAACGGCTTCGTT	19896
Db	8807	GTCGCTCAAAACACCCCTTCCTCCGACCTTCGCACACAAACACAGTTAACGGCTTCGTT	8866
QY	19897	AGATGACGTTTATTTATTTATTTATTTATTAATCATAGCTATTTGGCGGGCGCCGTCGCCAA	19956
Db	8867	AGATGACGTTTATTTATTTATTTATTTATTTATTAATCATAGCTATTTGGCGGGCGCCGTCGCCAA	8926
QY	19957	AAACATCTGTAAGATATTTCCAGTATTTGGAAACCGGCTGGAAACAACGTCCTCCGGGGCTCTG	20016
Db	8927	AAACATCTGTAAGATATTTCCAGTATTTGGAAACCGGCTGGAAACAACGTCCTCCGGGGCTCTG	8986
QY	20017	CCCTCCCAACGACGACGAGGTTTTTTCATTTAGACTCCGGGACACCTATTTTGTATTTAC	20076
Db	8987	CCCTCCCAACGACGACGAGGTTTTTTCATTTAGACTCCGGGACACCTATTTTGTATTTAC	9046
QY	20077	GGAAGACTCTCTCAATTAGAGAGTTCGAGGGGGGGAACAGACACAGGTACCCGCGGAGCCAT	20136
Db	9047	GGAAGACTCTCTCAATTAGAGAGTTCGAGGGGGGGAACAGACACAGGTACCCGCGGAGCCAT	9106
QY	20137	GGCGCGGGGCTCCGGCGCTCCCGGGGGCGGTCTCAGACAGCTCTCAATGCTGCTAGGTA	20196
Db	9107	GGCGCGGGGCTCCGGCGCTCCCGGGGGCGGTCTCAGACAGCTCTCAATGCTGCTAGGTA	9166
QY	20197	ACTCTCTAGAGCCCGGAGCCCGGGAACATAGGGCTCATACACTCGGGCCCGCGAAACTC	20256
Db	9167	ACTCTCTAGAGCCCGGAGCCCGGGAACATAGGGCTCATACACTCGGGCCCGCGAAACTC	9226
QY	20257	GGGGCGCTGGCACTCAACGTTTAGACATCAATATATGGAAGTGAACAACAGCATGATGGC	20316
Db	9227	GGGGCGCTGGCACTCAACGTTTAGACATCAATATATGGAAGTGAACAACAGCATGATGGC	9286
QY	20317	CGGGTACTCAGCAACCCGACAGAGAGTGGATGGTGGCACAGGTAAACGACACCGCTG	20376
Db	9287	CGGGTACTCAGCAACCCGACAGAGAGTGGATGGTGGCACAGGTAAACGACACCGCTG	9346
QY	20377	TATGTTAAACCCCACTTTCAGACAGGGGCCCTCGGTGCTGTAAGAAGAGCGCGGTTGCC	20436
Db	9347	TATGTTAAACCCCACTTTCAGACAGGGGCCCTCGGTGCTGTAAGAAGAGCGCGGTTGCC	9406
QY	20437	GGCCCACTGGGGGAGACGTTAATTTCCAGCGGCACTCGGGGGAGGCGCCAGCGTAGGGCT	20496
Db	9407	GGCCCACTGGGGGAGACGTTAATTTCCAGCGGCACTCGGGGGAGGCGCCAGCGTAGGGCT	9466
QY	20497	GGCGCGCCCAACAGACAGGTAAATAACAAGACGACAGACAGGGAACATGACCGTTAAT	20556
Db	9467	GGCGCGCCCAACAGACAGGTAAATAACAAGACGACAGACAGGGAACATGACCGTTAAT	9526
QY	20557	TACTCGGTTCAATTCGCGGGCGGGCGGGTCAAGCCGAGGTCCATTTAAAAACAACGG	20616
Db	9527	TACTCGGTTCAATTCGCGGGCGGGCGGGTCAAGCCGAGGTCCATTTAAAAACAACGG	9586
QY	20617	CCGCAACCCCAACAGCGGGGGCGCGCCCTCGGAACGCGGTTCTTCCATATGCCAAGAAC	20676
Db	9587	CCGCAACCCCAACAGCGGGGGCGCGCCCTCGGAACGCGGTTCTTCCATATGCCAAGAAC	9646
QY	20677	CGCGTACAAAAAGGCGCTGTTTGAACCATTTTGTGCCATCGGGGTTCTGTTTCAAT	20736

Accession	LOCUS	DEFINITION	KEYWORDS	ORGANISM	REFERENCE	AUTHORS	TITLE
Db	9647	CGCGTCACAAAAGGGCTCGTTTGAACCCATTTTGTGCCATCGGGTTTCGTTTCAGAT					
QY	20737	ACGGAAACGGCTCGTCCAAAAACACCCAAACGGGGGTGTGCTCAAAAGGCCATCTCATCT					
Db	9707	ACGGAAACGGCTCGTCCAAAAACACCCAAACGGGGGTGTGCTCAAAAGGCCATCTCATCT					
QY	20797	CTATGTGGGGATGGGGGTCTGTAAGCCCTTGACACTCAGATCCGGCCGGCTAAAGTCTTCCA					
Db	9767	CTATGTGGGGATGGGGGTCTGTAAGCCCTTGACACTCAGATCCGGCCGGCTAAAGTCTTCCA					
QY	20857	GACGGCCACCTTCTCTCAAAATCTTACGCCCGGAAAGGACGGGGGTCTCTCCGACGT					
Db	9827	GACGGCCACCTTCTCTCAAAATCTTACGCCCGGAAAGGACGGGGGTCTCTCCGACGT					
QY	20917	GAAGCAGCAGGGGATCAACAGTGGTTGTTTAAACGTGGGGCTCACCAAGGTGTGCACAA					
Db	9887	GAAGCAGCAGGGGATCAACAGTGGTTGTTTAAACGTGGGGCTCACCAAGGTGTGCACAA					
QY	20977	AGTCTCCCGGGGTCAAGCCCGCTGACGTGAGCGATGATACGTACGAGAGGGCGTAGCTGG					
Db	9947	AGTCTCCCGGGGTCAAGCCCGCTGACGTGAGCGATGATACGTACGAGAGGGCGTAGCTGG					
QY	21037	CGATGTTAAAGGGGACCCCGAGGGCCATGTCGGGGGACCTTGCTACAGCTGGGAGGACA					
Db	10007	CGATGTTAAAGGGGACCCCGAGGGCCATGTCGGGGGACCTTGCTACAGCTGGGAGGACA					
QY	21097	GCTCTCCCCCGAGCCACGTAAAACTGACACAAACGTTAGACAAAGAGGAGAGACCATCCGC					
Db	10067	GCTCTCCCCCGAGCCACGTAAAACTGACACAAACGTTAGACAAAGAGGAGAGACCATCCGC					
QY	21157	CGAGGTCCGGGGGTCTCCACGCGCATATACGATGCGCGATGCTGGGGCCCGCTGTAA					
Db	10127	CGAGGTCCGGGGGTCTCCACGCGCATATACGATGCGCGCGATGCTGGGGCCCGCTGTAA					
QY	21217	TTAATATCCACACGTAAACGACGTGGTGCACCCCTGATCCCTGTACTGTGGCGTGGGCC					
Db	10187	TTAATATCCACACGTAAACGACGTGGTGCACCCCTGATCCCTGTACTGTGGCGTGGGCC					
QY	21277	CCCTGTACTCCGCGCCCAAAATGTCTCCACTGGAACCCCGTACACCGGCCCGCAGATGCGCT					
Db	10247	CCCTGTACTCCGCGCCCAAAATGTCTCCACTGGAACCCCGTACACCGGCCCGCAGATGCGCT					
QY	21337	CGCGGGCGGTCCCGGAGACGCTCGCGCGCGCCAAAGGCGCGGGA					
Db	10307	CGCGGGCGGTCCCGGAGACGCTCGCGCGCGCCAAAGGCGCGGGA					
RESULT 4	AF087411	3804 bp DNA linear VRL 04-NOV-1999					
LOCUS	AF087411	Rhesus macaque rhadinovirus R2 protein, thymidylate synthase, and					
DEFINITION	AF087411	R3 protein genes, complete cds.					
ACCESSION	AF087411.1	GI:5823013					
KEYWORDS							
SOURCE							
ORGANISM							
REFERENCE							
AUTHORS							
TITLE							
JOURNAL							
MEDLINE							
PUBMED							
REFERENCE							
AUTHORS							
TITLE							

JOURNAL Submitted (26-Aug-1998) Division of Pathobiology and Immunology,
Oregon Health Sciences University / Oregon Regional Primate
Research Center, 505 NW 185th Avenue, Beaverton, OR 97006, USA

FEATURES

Location/Qualifiers

1..3804

/organism="Cercopithecine herpesvirus 17"

/mol_type="genomic DNA"

/db_xref="taxon:154334"

complement(519..1142)

/note="similar to Interleukin-6"

/codon_start=1

/product="R2 protein"

/protein_id="A053008.1"

/db_xref="GI:5823014"

/translation="MRPVFVFLYSCMAAPLPAAPPTAAGINVLPMONASLR
TRGRLEVGNTIDRMFYLCNHSTLCVREYPRIMSVHPIIMSNVECRREKGE
CMNAVRGLRAESYLRMLDLDDAGDDAAAGSALVIVLSALDSLIEELPVNK
IGGAESNEKTVRALGGSPRDVYLSARILEYLOMFRLDRRAIAM"

complement(1375..2376)

/note="ORF70"

/codon_start=1

/product="thymidylate synthase"

/protein_id="A053009.1"

/db_xref="GI:5823015"

/translation="MIVVHLGICVYKRIIPVCAGIAARLRFVSAPEGAARVAC
RGHGELOYLAHLDLIKHGVRDRTGTVRSVGLQARYNDEPEPLTRKFMWR
GVYELMIRGSTSTELSRGKYMIDAGSRAFLAAGRREDDLPYGFQWR
HFGAEYRGADANEGGVDRLRYVDLINRPHDRIVYKMANPADARALPCHYL
CQFVAVAGELSCQYQISADMGISVPINISVALTYLIAHVGLTGVDVHLGDH
VYNNHVDPLLOLRTPRPPLRLIKLVARLDEFTRADLSLEGDPHPIEMEMAV"

complement(2843..3190)

/note="similar to MIP"

/codon_start=1

/product="R3 protein"

/protein_id="A053010.1"

/db_xref="GI:5823016"

/translation="MRGLFVCFVFAFVACVVDYAFPMGSMGPAPELCLGYTHLP
PGLVSVSHTSQCSVDVILNTRGRKILCANPDDAVKLLQAVDRPKRGRTRRS
LIDSEKGLSGS"

complement(2843..3190)

/note="similar to MIP"

/codon_start=1

/product="R3 protein"

/protein_id="A053010.1"

/db_xref="GI:5823016"

/translation="MRGLFVCFVFAFVACVVDYAFPMGSMGPAPELCLGYTHLP
PGLVSVSHTSQCSVDVILNTRGRKILCANPDDAVKLLQAVDRPKRGRTRRS
LIDSEKGLSGS"

complement(2843..3190)

/note="similar to MIP"

/codon_start=1

/product="R3 protein"

/protein_id="A053010.1"

/db_xref="GI:5823016"

/translation="MRGLFVCFVFAFVACVVDYAFPMGSMGPAPELCLGYTHLP
PGLVSVSHTSQCSVDVILNTRGRKILCANPDDAVKLLQAVDRPKRGRTRRS
LIDSEKGLSGS"

complement(2843..3190)

/note="similar to MIP"

/codon_start=1

/product="R3 protein"

/protein_id="A053010.1"

/db_xref="GI:5823016"

/translation="MRGLFVCFVFAFVACVVDYAFPMGSMGPAPELCLGYTHLP
PGLVSVSHTSQCSVDVILNTRGRKILCANPDDAVKLLQAVDRPKRGRTRRS
LIDSEKGLSGS"

complement(2843..3190)

/note="similar to MIP"

/codon_start=1

/product="R3 protein"

/protein_id="A053010.1"

/db_xref="GI:5823016"

/translation="MRGLFVCFVFAFVACVVDYAFPMGSMGPAPELCLGYTHLP
PGLVSVSHTSQCSVDVILNTRGRKILCANPDDAVKLLQAVDRPKRGRTRRS
LIDSEKGLSGS"

complement(2843..3190)

/note="similar to MIP"

/codon_start=1

/product="R3 protein"

/protein_id="A053010.1"

/db_xref="GI:5823016"

/translation="MRGLFVCFVFAFVACVVDYAFPMGSMGPAPELCLGYTHLP
PGLVSVSHTSQCSVDVILNTRGRKILCANPDDAVKLLQAVDRPKRGRTRRS
LIDSEKGLSGS"

complement(2843..3190)

/note="similar to MIP"

/codon_start=1

/product="R3 protein"

/protein_id="A053010.1"

/db_xref="GI:5823016"

/translation="MRGLFVCFVFAFVACVVDYAFPMGSMGPAPELCLGYTHLP
PGLVSVSHTSQCSVDVILNTRGRKILCANPDDAVKLLQAVDRPKRGRTRRS
LIDSEKGLSGS"

complement(2843..3190)

/note="similar to MIP"

/codon_start=1

/product="R3 protein"

/protein_id="A053010.1"

/db_xref="GI:5823016"

/translation="MRGLFVCFVFAFVACVVDYAFPMGSMGPAPELCLGYTHLP
PGLVSVSHTSQCSVDVILNTRGRKILCANPDDAVKLLQAVDRPKRGRTRRS
LIDSEKGLSGS"

complement(2843..3190)

/note="similar to MIP"

/codon_start=1

/product="R3 protein"

/protein_id="A053010.1"

/db_xref="GI:5823016"

/translation="MRGLFVCFVFAFVACVVDYAFPMGSMGPAPELCLGYTHLP
PGLVSVSHTSQCSVDVILNTRGRKILCANPDDAVKLLQAVDRPKRGRTRRS
LIDSEKGLSGS"

complement(2843..3190)

/note="similar to MIP"

/codon_start=1

/product="R3 protein"

/protein_id="A053010.1"

/db_xref="GI:5823016"

/translation="MRGLFVCFVFAFVACVVDYAFPMGSMGPAPELCLGYTHLP
PGLVSVSHTSQCSVDVILNTRGRKILCANPDDAVKLLQAVDRPKRGRTRRS
LIDSEKGLSGS"

complement(2843..3190)

/note="similar to MIP"

/codon_start=1

/product="R3 protein"

/protein_id="A053010.1"

/db_xref="GI:5823016"

/translation="MRGLFVCFVFAFVACVVDYAFPMGSMGPAPELCLGYTHLP
PGLVSVSHTSQCSVDVILNTRGRKILCANPDDAVKLLQAVDRPKRGRTRRS
LIDSEKGLSGS"

complement(2843..3190)

/note="similar to MIP"

/codon_start=1

/product="R3 protein"

/protein_id="A053010.1"

/db_xref="GI:5823016"

/translation="MRGLFVCFVFAFVACVVDYAFPMGSMGPAPELCLGYTHLP
PGLVSVSHTSQCSVDVILNTRGRKILCANPDDAVKLLQAVDRPKRGRTRRS
LIDSEKGLSGS"

complement(2843..3190)

/note="similar to MIP"

/codon_start=1

/product="R3 protein"

/protein_id="A053010.1"

/db_xref="GI:5823016"

/translation="MRGLFVCFVFAFVACVVDYAFPMGSMGPAPELCLGYTHLP
PGLVSVSHTSQCSVDVILNTRGRKILCANPDDAVKLLQAVDRPKRGRTRRS
LIDSEKGLSGS"

complement(2843..3190)

/note="similar to MIP"

/codon_start=1

/product="R3 protein"

/protein_id="A053010.1"

/db_xref="GI:5823016"

/translation="MRGLFVCFVFAFVACVVDYAFPMGSMGPAPELCLGYTHLP
PGLVSVSHTSQCSVDVILNTRGRKILCANPDDAVKLLQAVDRPKRGRTRRS
LIDSEKGLSGS"

complement(2843..3190)

/note="similar to MIP"

/codon_start=1

/product="R3 protein"

/protein_id="A053010.1"

/db_xref="GI:5823016"

/translation="MRGLFVCFVFAFVACVVDYAFPMGSMGPAPELCLGYTHLP
PGLVSVSHTSQCSVDVILNTRGRKILCANPDDAVKLLQAVDRPKRGRTRRS
LIDSEKGLSGS"

complement(2843..3190)

/note="similar to MIP"

/codon_start=1

/product="R3 protein"

/protein_id="A053010.1"

/db_xref="GI:5823016"

/translation="MRGLFVCFVFAFVACVVDYAFPMGSMGPAPELCLGYTHLP
PGLVSVSHTSQCSVDVILNTRGRKILCANPDDAVKLLQAVDRPKRGRTRRS
LIDSEKGLSGS"

complement(2843..3190)

/note="similar to MIP"

/codon_start=1

/product="R3 protein"

/protein_id="A053010.1"

/db_xref="GI:5823016"

/translation="MRGLFVCFVFAFVACVVDYAFPMGSMGPAPELCLGYTHLP
PGLVSVSHTSQCSVDVILNTRGRKILCANPDDAVKLLQAVDRPKRGRTRRS
LIDSEKGLSGS"

complement(2843..3190)

/note="similar to MIP"

/codon_start=1

/product="R3 protein"

/protein_id="A053010.1"

/db_xref="GI:5823016"

/translation="MRGLFVCFVFAFVACVVDYAFPMGSMGPAPELCLGYTHLP
PGLVSVSHTSQCSVDVILNTRGRKILCANPDDAVKLLQAVDRPKRGRTRRS
LIDSEKGLSGS"

complement(2843..3190)

/note="similar to MIP"

/codon_start=1

/product="R3 protein"

/protein_id="A053010.1"

/db_xref="GI:5823016"

/translation="MRGLFVCFVFAFVACVVDYAFPMGSMGPAPELCLGYTHLP
PGLVSVSHTSQCSVDVILNTRGRKILCANPDDAVKLLQAVDRPKRGRTRRS
LIDSEKGLSGS"

complement(2843..3190)

/note="similar to MIP"

/codon_start=1

/product="R3 protein"

/protein_id="A053010.1"

/db_xref="GI:5823016"

/translation="MRGLFVCFVFAFVACVVDYAFPMGSMGPAPELCLGYTHLP
PGLVSVSHTSQCSVDVILNTRGRKILCANPDDAVKLLQAVDRPKRGRTRRS
LIDSEKGLSGS"

complement(2843..3190)

/note="similar to MIP"

/codon_start=1

/product="R3 protein"

/protein_id="A053010.1"

/db_xref="GI:5823016"

/translation="MRGLFVCFVFAFVACVVDYAFPMGSMGPAPELCLGYTHLP
PGLVSVSHTSQCSVDVILNTRGRKILCANPDDAVKLLQAVDRPKRGRTRRS
LIDSEKGLSGS"

complement(2843..3190)

/note="similar to MIP"

/codon_start=1

/product="R3 protein"

/protein_id="A053010.1"

/db_xref="GI:5823016"

/translation="MRGLFVCFVFAFVACVVDYAFPMGSMGPAPELCLGYTHLP
PGLVSVSHTSQCSVDVILNTRGRKILCANPDDAVKLLQAVDRPKRGRTRRS
LIDSEKGLSGS"

complement(2843..3190)

/note="similar to MIP"

/codon_start=1

/product="R3 protein"

/protein_id="A053010.1"

/db_xref="GI:5823016"

/translation="MRGLFVCFVFAFVACVVDYAFPMGSMGPAPELCLGYTHLP
PGLVSVSHTSQCSVDVILNTRGRKILCANPDDAVKLLQAVDRPKRGRTRRS
LIDSEKGLSGS"

complement(2843..3190)

/note="similar to MIP"

/codon_start=1

/product="R3 protein"

/protein_id="A053010.1"

/db_xref="GI:5823016"

/translation="MRGLFVCFVFAFVACVVDYAFPMGSMGPAPELCLGYTHLP
PGLVSVSHTSQCSVDVILNTRGRKILCANPDDAVKLLQAVDRPKRGRTRRS
LIDSEKGLSGS"

complement(2843..3190)

/note="similar to MIP"

/codon_start=1

/product="R3 protein"

/protein_id="A053010.1"

/db_xref="GI:5823016"

/translation="MRGLFVCFVFAFVACVVDYAFPMGSMGPAPELCLGYTHLP
PGLVSVSHTSQCSVDVILNTRGRKILCANPDDAVKLLQAVDRPKRGRTRRS
LIDSEKGLSGS"

complement(2843..3190)

/note="similar to MIP"

/codon_start=1

/product="R3 protein"

/protein_id="A053010.1"

/db_xref="GI:5823016"

/translation="MRGLFVCFVFAFVACVVDYAFPMGSMGPAPELCLGYTHLP
PGLVSVSHTSQCSVDVILNTRGRKILCANPDDAVKLLQAVDRPKRGRTRRS
LIDSEKGLSGS"

complement(2843..3190)

/note="similar to MIP"

/codon_start=1

/product="R3 protein"

/protein_id="A053010.1"

/db_xref="GI:5823016"

/translation="MRGLFVCFVFAFVACVVDYAFPMGSMGPAPELCLGYTHLP
PGLVSVSHTSQCSVDVILNTRGRKILCANPDDAVKLLQAVDRPKRGRTRRS
LIDSEKGLSGS"

complement(2843..3190)

/note="similar to MIP"

/codon_start=1

/product="R3 protein"

/protein_id="A053010.1"

/db_xref="GI:5823016"

/translation="MRGLFVCFVFAFVACVVDYAFPMGSMGPAPELCLGYTHLP
PGLVSVSHTSQCSVDVILNTRGRKILCANPDDAVKLLQAVDRPKRGRTRRS
LIDSEKGLSGS"

complement(2843..3190)

/note="similar to MIP"

/codon_start=1

/product="R3 protein"

/protein_id="A053010.1"

/db_xref="GI:5823016"

/translation="MRGLFVCFVFAFVACVVDYAFPMGSMGPAPELCLGYTHLP
PGLVSVSHTSQCSVDVILNTRGRKILCANPDDAVKLLQAVDRPKRGRTRRS
LIDSEKGLSGS"

complement(2843..3190)

/note="similar to MIP"

/codon_start=1

OY	20903	GGTCTCCGACGCTGAAAGCAGCAGGAGATCAAGCTGTTTGTGTAACGTGGCGTCACC	20962
Db	1501	GGCTCTCCGACGCTGAAAGCAGCAGGAGATCAAGCTGTTTGTGTAACGTGGCGTCACC	1560
OY	20963	CAAGGTGACCAAAAGCTCCCGGGGTCCAGGCCGTACGTGAGCGCATCAGATACGTCAG	21022
Db	1561	CAAGGTGACCAAAAGCTCCCGGGGTCCAGGCCGTACGTGAGCGCATCAGATACGTCAG	1620
OY	21023	GAGGGCGTAGCTGGCGATGTTTAAACGGGACCCCGAGGCCCTMTCTGGCGAGACTCTGTA	21082
Db	1621	GAGGGCGTAGCTGGCGATGTTTAAACGGGACCCCGAGGCCCTMTCTGGCGAGACTCTGTA	1680
OY	21083	CAGCTGGCAGACAGCTCTCCCGCGAGCAGCTAAACTGACACAAAAGTGCACAGAGAG	21142
Db	1681	CAGCTGGCAGACAGCTCTCCCGCGAGCAGCTAAACTGACACAAAAGTGCACAGAGAG	1740
OY	21143	GAGAGCCATCCGCGCAGAGTCCGGGGGGTCCACGGGCATATAGCATGGCGGATCGAG	21202
Db	1741	GAGAGCCATCCGCGCAGAGTCCGGGGGGTCCACGGGCATATAGCATGGCGGATCGAG	1800
OY	21203	GGGCGCGCTGTTAATTAGATCCACACAGTAACGACAGTGGTCCACCCTCGACCTTCGTA	21262
Db	1801	GGGCGCGCTGTTAATTAGATCCACACAGTAACGACAGTGGTCCACCCTCGACCTTCGTA	1860
OY	21263	GTGTGGCGTGGCCCCCTGTACTCCGCCCCCAAAATGCTCTCACTGGAACCCGTACACGG	21322
Db	1861	GTGTGGCGTGGCCCCCTGTACTCCGCCCCCAAAATGCTCTCACTGGAACCCGTACACGG	1920
OY	21323	CCCCAGATGCGCCCTCGGGGGGGTCCCGAAGCCCTCGCGGCCCAAAAAGGCGGGGACCC	21382
Db	1921	CCCCAGATGCGCCCTCGGGGGGGTCCCGAAGCCCTCGCGGCCCAAAAAGGCGGGGACCC	1980
OY	21383	GTGGCGCTCCCAATTTTATAGCCCGCGGCACGACAGTGTGGTGGATCGGTGGAGCCCT	21442
Db	1981	GTGGCGCTCCCAATTTTATAGCCCGCGGCACGACAGTGTGGTGGATCGGTGGAGCCCT	2040
OY	21443	GATTAACCAACGACACTCTCTCCACAGACGCCCTCCCAAAACCCCTTTGGTGGTAAACAG	21502
Db	2041	GATTAACCAACGACACTCTCTCCACAGACGCCCTCCCAAAACCCCTTTGGTGGTAAACAG	2100
OY	21503	AGAAACATCGCCCTGAGGTATATGAGGGGCTGAACCCGAAACAGGACCTGGTGGCCAC	21562
Db	2101	AGAAACATCGCTCCCTGAGGTATATGAGGGGCTGAACCCGAAACAGGACCTGGTGGCCAC	2160
OY	21563	GCCCCGCTCTCCTCCCTCTGCACAGCGCTGTATTAATTAATTAATCCAGGTGCGCCAAATTA	21622
Db	2161	GCCCCGCTCTCCTCCCTCTGCACAGCGCTGTATTAATTAATTAATTAATCCAGGTGCGCCAAATTA	2220
OY	21623	CTGACAGCTCGCCGTGGTTCGCCCGCGGCACAGCGACGGCGAGCGCGCGGCACCTTCGGGTGC	21682
Db	2221	CTGACAGCTCGCCGTGGTTCGCCCGCGGCACAGCGACGGCGAGCGCGCGGCACCTTCGGGTGC	2280
OY	21683	GGAAAAAACC CGGAGTGTGTCGGCGCGGAGTTCACAGCAGCAAGCGGGATTAATTTTTTT	21742
Db	2281	GGAAAAAACC CGGAGTGTGTCGGCGCGGAGTTCACAGCAGCAAGCGGGATTAATTTTTTT	2340
OY	21743	AACGTACAGATACCGAGATGACACAGGACAATCATATTTAGCAACCGAGAGTCTTTACAA	21802
Db	2341	AACGTACAGATACCGAGATGACACAGGACAATCATATTTAGCAACCGAGAGTCTTTACAA	2400
OY	21803	CTATTAACCGTAAACGGCTGTAAGACGAATCTTATTTTAAAGCAGCTTGGCGGGCGCGAC	21862
Db	2401	CTATTAACCGTAAACGGCTGTAAGACGAATCTTATTTTAAAGCAGCTTGGCGGGCGCGAC	2460
OY	21863	CACAGGGGGGGCGCGGTGTATACGAGTATATAACCCAGGTGTCTCCCAAGCTGTCC	21922
Db	2461	CACAGGGGGGGCGCGGTGTATACGAGTATATAACCCAGGTGTCTCCCAAGCTGTCC	2520
OY	21923	CCGAGCGTGAAGCTGTCTCCCAACGGCCAAAACACACAGATTAATTAATTAATTAACATG	21982
Db	2521	CCGAGCGTGAAGCTGTCTCCCAACGGCCAAAACACACAGATTAATTAATTAATTAACATG	2580
OY	21983	TTTATTTTATTAACCTTAACGGCGCATTAATGCTTCTTAACAGGGGCCAATGAAGCAAC	22042

Db	2581	TTTTATTTTTTTTAAACCTTAACGCGCGATTAAGCTTTTAAACAGGGGCGCAATAGAACAC	2640
QY	22043	GTGGCAGGCGGCAATTCGCGCGCTCAAAAGCAACGCAACCGGCGCTCGTAACAGCGTA	2210:
Db	2641	GTGGCAGGCGGCAATTCGCGCGCTCAAAAGCAACGCAACCGGCGCTCGTAACAGCGTA	2700
QY	22103	AACAAACAATATTAGCCATTCTGAATCCGTAATAATCCAAACCCCTCTGCGCTCCGAGCAATT	2216:
Db	2701	AACAACAATATTAGCCATTCTGAATCCGTAATAATCCAAACCCCTCTGCGCTCCGAGCAATT	2760
QY	22163	CGCCACGCTGGGCTCTACGTCCAGGGGTGTTTAAAGTCGCAATTTTGACCTTGGCAGCGC	2222:
Db	2761	CGCCACGCTGGGCTCTACGTCCAGGGGTGTTTAAAGTCGCAATTTTGACCTTGGCAGCGC	2820
QY	22223	GCGGCTCGGTTAAATGGTTTCTAAATCCCGCTGCAAGAGGCCCTCTTGGAAATCGCAAC	2228:
Db	2821	GCGGCTCGGTTAAATGGTTTCTAAATCCCGCTGCAAGAGGCCCTCTTGGAAATCGCAAC	2880
QY	22283	TCAGGCTCGGCGGGGTTCTTCGCCCTTTTGGGAGCGTTGTCACCGCCCTGAAGCAGTT	2234:
Db	2881	TCAGGCTCGGCGGGGTTCTTCGCCCTTTTGGGAGCGTTGTCACCGCCCTGAAGCAGTT	2940
QY	22343	TCCTTACAGCGCTCGTCCCCGGGATTGGCAGACAGCTTTTACCGCGGCGAGTGTTTAATA	2240:
Db	2941	TCCTTACAGCGCTCGTCCCCGGGATTGGCAGACAGCTTTTACCGCGGCGAGTGTTTAATA	3000
QY	22403	TCACGCGCTCCACGAGAGCTGCGACGAGGTGTGGAGTAAAGACCACTTAACCGGGGTG	2246:
Db	3001	TCACGCGCTCCACGAGAGCTGCGACGAGGTGTGGAGTAAAGACCACTTAACCGGGGTG	3060
QY	22463	GCGGAGATGAGTTACATATACCCCAACAGCAGAGTTTGGGGCGGGGTCCGCTCATGGAGC	2252:
Db	3061	GCGGAGATGAGTTACATATACCCCAACAGCAGAGTTTGGGGCGGGGTCCGCTCATGGAGC	3120
QY	22523	CCATTAAGAAAGGCATTAATCAACTACACACGCGAACCCTGCAAAAAAAGCCACACGAAAA	2258:
Db	3121	CCATTAAGAAAGGCATTAATCAACTACACACGCGAACCCTGCAAAAAAAGCCACACGAAAA	3180
QY	22583	GGCCCCATATGTTGACAAAAACAACAAAAAGAGGGGTGCGCTCGTGGCTTGCACACAG	2264:
Db	3181	GGCCCCATATGTTGACAAAAACAACAAAAAGAGGGGTGCGCTCGTGGCTTGCACACAG	3240
QY	22643	CGCCACGCTCGCGTGCTGGGCGACGGGTGAAGGGCGCTCATTAATACCGCGGCGCGGGC	2270:
Db	3241	CGCCACGCTCGCGTGCTGGGCGACGGGTGAAGGGCGCTCATTAATACCGCGGCGCGGGC	3300
QY	22703	CCGCGCTCGACGGAAACAGGGGTGTGTAAGCAGCTACGACAGTGGCTCCCGTCCAGATG	2276:
Db	3301	CCGCGCTCGACGGAAACAGGGGTGTGTAAGCAGCTACGACAGTGGCTCCCGTCCAGATG	3360
QY	22763	TGGCATTCGAGTCCCAAAAGGGGCGTGTAACTAAGTGGCGCCCGGGGTGTAAAGAAC	2282:
Db	3361	TGGCATTCGAGTCCCAAAAGGGGCGTGTAACTAAGTGGCGCCCGGGGTGTAAAGAAC	3420
QY	22823	GGGGATCCCCAAACAGGTAAAAAGCTTTTGTCCAAACAGAAAAGCCACAGCAACCGAA	2288:
Db	3421	GGGGATCCCCAAACAGGTAAAAAGCTTTTGTCCAAACAGAAAAGCCACAGCAACCGAA	3480
QY	22883	AGGAATCTCCAAACAGCAAGGGTCCCGTGCAGGGCGATTAACAGGAAAAATTTCCCTCACG	2294:
Db	3481	AGGAATCTCCAAACAGCAAGGGTCCCGTGCAGGGCGATTAACAGGAAAAATTTCCCTCACG	3540
QY	22943	TAAACACACGCGCGCGTAACCTTTAAACACAGCAATACTTCTCGAGCCCTGTGTTAAT	2300:
Db	3541	TAAACACACGCGCGCGTAACCTTTAAACACAGCAATACTTCTCGAGCCCTGTGTTAAT	3600
QY	23003	AAAAACACAAAGGTTGTAAATTTTCGCGGGGCGCTTTGGGCGCCGCGCGTCTGGGGGTGGG	2306:
Db	3601	AAAAACACAAAGGTTGTAAATTTTCGCGGGGCGCTTTGGGCGCCGCGCGTCTGGGGGTGGG	3660
QY	23063	TTGTCTCGTTGTGGTTGCAATACCAACCCCGCTGCGGAAAAACAGGGCAACACCCC	2312:

Db 3661 TTGCTGCTGTTGCTGTCGCAATCAACACCCCGCTGCCGGAACAGGCAACACCCCC 3720
Oy 23123 TGGCGTAGTTTTTTAAAAAATTAACACCGGCGAGGAGAGGAGGAAGGGGTGGCGCTAA 23182
Db 3721 TGGCGTAGTTTTTTAAAAAATTAACACCGGCGAGGAGGAGGAGGAAGGGGTGGCGCTAA 3780
Oy 23183 ATGGGCTGTTAGACGCAACCGCA 23206
Db 3781 ATGGGCTGTTAGACGCAACCGCA 3804

RESULT 5
AF159033 475 bp DNA linear VRL 28-APR-2000
LOCUS Macaque gamma virus strain Macaca mulatta gamma virus DNA
DEFINITION polymerase (pol) gene, partial cds.
ACCESSION AF159033
VERSION AF159033.1 GI:6671074
KEYWORDS
SOURCE Macaque gamma virus
ORGANISM Macaque gamma virus
VIRUSES; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
REFERENCE 1 (bases 1 to 475)
AUTHORS Strand,K., Harper,E., Thormahlen,S., Thoulless,M.E., Tsai,C.,
Rose,T. and Bosch,M.L.
TITLE Two distinct lineages of macaque gamma herpesviruses related to the
J. Clin. Virol. 16 (3), 253-269 (2000)
MEDLINE 20204465
PUBMED 10738144
REFERENCE 2 (bases 1 to 475)
AUTHORS Strand,K.B. and Bosch,M.L.
TITLE Direct Submission
JOURNAL Submitted (14-JUN-1999) Pathobiology, University of Washington, Box
357238, Seattle, WA 98125, USA
FEATURES
source
1. 475
/organism="Macaque gamma virus"
/mol_type="genomic DNA"
/strain="Macaque mulatta gamma virus"
/db_xref="taxon:111468"
<1..>475
/gene="pol"
<1..>475
/gene="pol"
/codon_start=2
/product="DNA polymerase"
/protein_id="AAF23083.1"
/db_xref="GI:6671075"
/translation="SITQAHNLICSTMIHGRDLIHPNLTTPDQYETFLSGGPVHFVK
KHKRESILGRILTYMELKRRIRKTLACDDPSKTLIDKQOLAIKYTCNAYGCTGY
ASGLPCINIAIEVTLTKRTMLEMSKSYVALTEEDLTRILGREVTAHGAHFVYV"

BASE COUNT 110 a 141 c 143 g 81 t
ORIGIN

Query Match 1.2%; Score 475; DB 1; Length 475;
Best Local Similarity 100.0%; Pred. NO. 4.8e-268;
Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 15963 CTTGCACCCCACTGACGCCGCGAGCACTACGAGACGTTGCTGAGCGGCGGACCGGT 16022
Oy 15963 CTTGCACCCCACTGACGCCGCGAGCACTACGAGACGTTGCTGAGCGGCGGACCGGT 16022
Db 61 CCTGCACCCCACTGACGCCGCGAGCACTACGAGACGTTGCTGAGCGGCGGACCGGT 120
Oy 16023 ACATTTTGTAAAAAACAAGCGGAGTCTCTGCGGAAGACTGCTAACCGTGGTT 16082
Db 121 ACATTTTGTAAAAAACAAGCGGAGTCTCTCTGCGGAAGACTGCTAACCGTGGTT 180
Oy 16083 AGAAAGCGAAGGCGATCCGGCGCACCTGGCGCGTGCATGACCCGTGCTAAAAAC 16142

Db 181 AGAAAGCGAAGGCGATCCGGCGACCCCTGGCGCGGTGCATGACCCGCTGCTAAAAAC 240
Oy 16143 CATCTTAGATTAACAACAGCTGGCGCATCAAGTACATGTAAACGGGTTTACGGGTTAC 16202
Db 241 CATCTTAGATTAACAACAGCTGGCGCATCAAGTACATGTAAACGGGTTTACGGGTTAC 300
Oy 16203 CGGGGTGGCCAGCGGCGCTCTCCCATGATTAACATAGCGAACCAGGAGCTCCGGGG 16262
Db 301 CGGGGTGGCCAGCGGCGCTCTCTCCCATGATTAACATAGCGAACCAGGAGCTCCGGGG 360
Oy 16263 GCGCAGATGCTGAGATGTCAAAGTCTTACGTGAGGCGCTGACGAGGAAGACTGCG 16322
Db 361 GCGCAGATGCTGAGATGTCAAAGTCTTACGTGAGGCGCTGACGAGGAAGACTGCG 420
Oy 16323 AACGCTCTCGGTGCGGACGAGTGACCGCCGTCACGCGCGGTTTCCGCTGCTC 16377
Db 421 AACGCTCTCGGTGCGGACGAGTGACCGCCGTCACGCGCGGTTTCCGCTGCTC 475

RESULT 6
AF159041 395 bp DNA linear VRL 28-APR-2000
LOCUS Macaque gamma virus strain Macaca mulatta gamma virus glycoprotein
DEFINITION B (gB) gene, partial cds.
ACCESSION AF159041
VERSION AF159041.1 GI:6671090
KEYWORDS
SOURCE Macaque gamma virus
ORGANISM Macaque gamma virus
VIRUSES; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
REFERENCE 1 (bases 1 to 395)
AUTHORS Strand,K., Harper,E., Thormahlen,S., Thoulless,M.E., Tsai,C.,
Rose,T. and Bosch,M.L.
TITLE Two distinct lineages of macaque gamma herpesviruses related to the
J. Clin. Virol. 16 (3), 253-269 (2000)
MEDLINE 20204465
PUBMED 10738144
REFERENCE 2 (bases 1 to 395)
AUTHORS Strand,K.B. and Bosch,M.L.
TITLE Direct Submission
JOURNAL Submitted (14-JUN-1999) Pathobiology, University of Washington, Box
357238, Seattle, WA 98125, USA
FEATURES
source
1. 395
/organism="Macaque gamma virus"
/mol_type="genomic DNA"
/strain="Macaque mulatta gamma virus"
/db_xref="taxon:111468"
<1..>395
/gene="gB"
<1..>395
/gene="gB"
/codon_start=3
/product="glycoprotein B"
/protein_id="AAF23091.1"
/db_xref="GI:6671091"
/translation="GTEDKTHQECILWFKKNIVPHIFKVRKRVATSVTVRGKTE
TAVYGKQEVIRPVPQYEINHMDFTYOCFSSSRVAVNGIVNTYTRDPTNCFVFLQPE
GLNDINIRYSOPPLTYTPGMFPGIYVR"

BASE COUNT 106 a 113 c 108 g 68 t
ORIGIN

Query Match 0.8%; Score 331; DB 1; Length 395;
Best Local Similarity 99.7%; Pred. NO. 3.3e-183;
Matches 381; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 11759 CGGCGACCGAGACAGACGACCAAGAGCATCTGATGCTTTTAAAAAATATTTG 11818
Db 1 CGGCGACCGAGACAGACGACCAAGAGCATCTGATGCTTTTAAAAAATATTTG 60

QY	11834	AGGTCAACAGCGTACCCGAAGGTGGCCACCTTCGGTACCGCTCTATCGAGGGTGGACCCAGA	1189
Db	1	AGGTCAACAGCGTACCCGAAGGTGGCCACCTTCGGTACCGCTCTATCGAGGGTGGACCCAGA	60
QY	11894	CCGCGCGTACCGGCAAGAGAGGTTCATCCGACCGGTGGCCAGTACGAGATCAACACCA	1195
Db	61	CCGCGCGTACCGGCAAGAGAGGTTCATCCGACCGGTGGCCAGTACGAGATCAACACCA	120
QY	11954	TGGACACGACCTACCAAGTGTTCGAGCTCCATGCGCGT	11990
Db	121	TGGACACGACCTACCAAGTGTTCGAGCTCCATGCGCGT	157
RESULT 8			
AF204167		2708 bp	DNA linear
LOCUS		Macaca nemestrina rhadinovirus 2	VRL 04-JUL-2000
DEFINITION		Macaca nemestrina rhadinovirus 2 DNA polymerase and ORF 10-like protein genes, partial cds.	
ACCESSION	AF204167		
VERSION	AF204167.1	GI:8925895	
KEYWORDS			
SOURCE		Macaca nemestrina rhadinovirus 2	
ORGANISM		Macaca nemestrina rhadinovirus 2	
REFERENCE		Viruses; dsDNA viruses, no RNA stage: Herpesviridae; Gammaherpesvirinae; Rhadinovirus.	
AUTHORS		1 (bases 1 to 2708) Schultz,E.R., Rankin,G.W. Jr., Blanc,M.P., Raden,B.W., Tsai,C.C. and Rose,T.M.	
TITLE		Characterization of two divergent lineages of macaque rhadinoviruses related to Kaposi's sarcoma-associated herpesvirus	
JOURNAL	J. Virol.	74 (10), 4919-4928	(2000)
MEDLINE	20240083		
PUBMED	10775636		
REFERENCE		2. (bases 1 to 2708) Rose,T.M.	
AUTHORS		Direct Submission	
TITLE		Submitted (12-NOV-1999) Pathobiology, School of Public Health and Community Medicine, University of Washington, Seattle, WA 98195,	
JOURNAL		USA	
FEATURES			
SOURCE			
CDS			
CDS			


```

BASE COUNT      559 a      852 c      811 g      486 t
ORIGIN
Query Match      0.2%; Score 80; DB 1; Length 2708;
Best Local Similarity 100.0%; Pred. No. 3.2e-35;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15703 CAGCCGAGCGCGCTCTGACGAGCGCCACACAGCTCCGCGTCTCTCGCTCTGAG 15762
Db 1126 CAGCCGAGCGCGCTCTGACGAGCGCCACACAGCTCCGCGTCTCTCGCTCTGAG 1185
OY 15763 GCCCGGCGCAGGAGAACTT 15782
Db 1186 GCCCGGCGCAGGAGAACTT 1205

RESULT 9
AF159031 475 bp DNA linear VRL 28-APR-2000
LOCUS Macaque gamma virus strain Macaca nemestrina gamma virus DNA
ACCESSION AF159031
VERSION AF159031.1 GI:6671070
KEYWORDS Macaque gamma virus
SOURCE Macaque gamma virus
ORGANISM Macaque gamma virus
VIRUSES: dsDNA viruses, no RNA stage; Herpesviridae;
REFERENCE 1 (bases 1 to 475)
AUTHORS Strand,K., Harper,E., Thormahlen,S., Thoulless,M.E., Tsai,C.,
TITLE Two distinct lineages of macaque gamma herpesviruses related to the
JOURNAL J. Clin. Virol. 16 (3), 253-269 (2000)
MEDLINE 20204465
PUBMED 10738144
REFERENCE 2 (bases 1 to 475)
AUTHORS Strand,K.B. and Bosch,M.L.
TITLE Direct Submission
JOURNAL Submitted (14-JUN-1999) Pathobiology, University of Washington, Box
357238, Seattle, WA 98125, USA
FEATURES
SOURCE Location/Qualifiers
1. 475
/organism="Macaque gamma virus"
/mol_type="genomic DNA"
/strain="Macaque nemestrina gamma virus"
/db_xref="taxon:111468"
<1..>475
/gene="pol"
<1..>475
/gene="pol"
<1..>475
/codon_start=2
/product="DNA polymerase"
/protein_id="AAF23081.1"
/db_xref="GI:6671071"
/translation="SITQAHNLCTSTIHGRDLHPPTLPDDYETVLSGGPVHFK
KHKRESLLGLRLTYWLEKRAIRRTLAACDDPSLKTIDKQOLAIKVNCNAVYGTGV
ASGLLPINIAETVTLGRRTMLEMSKYVEALITVSDRLRERLGRVTAAGPDAKFRV"
BASE COUNT 100 a 147 c 152 g 76 t
ORIGIN
Query Match 0.2%; Score 71; DB 1; Length 475;
Best Local Similarity 100.0%; Pred. No. 5.2e-30;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15903 GAGCATATCCAGCGGACACACTGTGCTACTCCACCATGTATACAGGAGAGACTTCA 15962
Db 1 GAGCATATCCAGCGGACACACTGTGCTACTCCACCATGTATACAGGAGAGACTTCA 60
OY 15963 CCTGACCCCA 15973

```

```

Db 61 CCTGACCCCA 71
RESULT 10
AF159034 336 bp DNA linear VRL 28-APR-2000
LOCUS Macaque gamma virus strain Macaca nemestrina 116 gamma virus DNA
DEFINITION Macaque gamma virus strain Macaca nemestrina 116 gamma virus DNA
ACCESSION AF159034
VERSION AF159034.1 GI:6671076
KEYWORDS Macaque gamma virus
SOURCE Macaque gamma virus
ORGANISM Macaque gamma virus
VIRUSES: dsDNA viruses, no RNA stage; Herpesviridae;
REFERENCE 1 (bases 1 to 336)
AUTHORS Strand,K., Harper,E., Thormahlen,S., Thoulless,M.E., Tsai,C.,
TITLE Two distinct lineages of macaque gamma herpesviruses related to the
JOURNAL J. Clin. Virol. 16 (3), 253-269 (2000)
MEDLINE 20204465
PUBMED 10738144
REFERENCE 2 (bases 1 to 336)
AUTHORS Strand,K.B. and Bosch,M.L.
TITLE Direct Submission
JOURNAL Submitted (14-JUN-1999) Pathobiology, University of Washington, Box
357238, Seattle, WA 98125, USA
FEATURES
SOURCE Location/Qualifiers
1. 336
/organism="Macaque gamma virus"
/mol_type="genomic DNA"
/strain="Macaque nemestrina 116 gamma virus"
/db_xref="taxon:111468"
<1..>336
/gene="pol"
<1..>336
/gene="pol"
<1..>336
/codon_start=2
/product="DNA polymerase"
/protein_id="AAF23084.1"
/db_xref="GI:6671077"
/translation="TMIHGRDLHPPTLPDDYETVLSGGPVHFKHKRESLLGLR
LTWLEKRAIRRTLAACDDPSLKTIDKQOLAIKVNCNAVYGTGVAAGLLPEINIA
ETVTLGRRT"
BASE COUNT 75 a 103 c 105 g 53 t
ORIGIN
Query Match 0.1%; Score 56; DB 1; Length 336;
Best Local Similarity 100.0%; Pred. No. 3.4e-21;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15976 CTGACGCCGCGACGACTACGAGACGTCGCTGAGCGCGGACCGTACATTGTGT 16031
Db 41 CTGACGCCGCGACGACTACGAGACGTCGCTGAGCGCGGACCGGTCATTGTGT 96

RESULT 11
AF159032 475 bp DNA linear VRL 28-APR-2000
LOCUS Macaque gamma virus strain Macaca fascicularis gamma virus DNA
DEFINITION Macaque gamma virus strain Macaca fascicularis gamma virus DNA
ACCESSION AF159032
VERSION AF159032.1 GI:6671072
KEYWORDS Macaque gamma virus
SOURCE Macaque gamma virus
ORGANISM Macaque gamma virus
VIRUSES: dsDNA viruses, no RNA stage; Herpesviridae;
REFERENCE 1 (bases 1 to 475)
AUTHORS Strand,K., Harper,E., Thormahlen,S., Thoulless,M.E., Tsai,C.,

```

TITLE Two distinct lineages of macaque gamma herpesviruses related to the
JOURNAL Kapoisi's sarcoma associated herpesvirus
MEDLINE J. Clin. Virol. 16 (3), 253-269 (2000)
PUBMED 20204465
10738144

REFERENCE 2 (bases 1 to 475)
AUTHORS Strand, K.B. and Bosch, M.L.
TITLE Direct Submission
JOURNAL Submitted (14-JUN-1999) Pathobiology, University of Washington, Box
357238, Seattle, WA 98125, USA

FEATURES
source Location/Qualifiers
1..475
/organism="Macaque gamma virus"
/mol_type="genomic DNA"
/strain="Macaque fascicularis gamma virus"
/db_xref="taxon:111468"
<1..>475
/gene="pol"
<1..>475
/gene="pol"
/codon_start=2
/product="DNA polymerase"
/protein_id="AA023082.1"
/db_xref="GI:6671073"
/translation="SIIQAHNLCYSTMHGDLHLPITLPDDYETFPVLSGGPVHFKV
HKHRSLSLGRITLWLEKRAIRRTLAACDDPSLTKITLQDLAKVTCNAVYGFYGV
ASGLPCINIAETVTLRGRTMLEMSKSYEATLTDLTRIGRVYTAGHGRFRV"

BASE COUNT 99 a 144 c 152 g 80 t

ORIGIN

Query Match 0.1%; Score 50; DB 1; Length 475;
Best Local Similarity 100.0%; Pred. No. 1.2e-17;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15903 GAGCATTCACGAGCGACACCTGCTGCTACATCCACCATGATACACGAC 15952
DB 1 GAGCATTCACGAGCGACACCTGCTGCTACATCCACCATGATACACGAC 50

RESULT 12
AF159036 336 bp DNA linear VRL 28-APR-2000
LOCUS Macaque gamma virus strain Macaca fascicularis 037 gamma virus DNA
DEFINITION Macaque gamma virus strain Macaca fascicularis 037 gamma virus DNA
ACCESSION AF159036
VERSION AF159036.1 GI:6671080
KEYWORDS Macaque gamma virus
SOURCE Macaque gamma virus
ORGANISM Macaque gamma virus
VIRUSES: dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
1 (bases 1 to 336)
/strain="Macaque fascicularis 040 gamma virus"
/db_xref="taxon:111468"
<1..>336
/gene="pol"
<1..>336
/gene="pol"
/codon_start=2
/product="DNA polymerase"
/protein_id="AA023087.1"
/db_xref="GI:6671083"
/translation="TWINGRDLHLPITLPDDYETFPVLSGGPVHFKHRSLSLGR
LTVLEKRAIRRTLAACDDPSLTKITLQDLAKVTCNAVYGFYGVASGLPCINIA
ETVTLRGRT"

TITLE Two distinct lineages of macaque gamma herpesviruses related to the
JOURNAL Kapoisi's sarcoma associated herpesvirus
MEDLINE J. Clin. Virol. 16 (3), 253-269 (2000)
PUBMED 20204465
10738144

REFERENCE 2 (bases 1 to 336)
AUTHORS Strand, K.B. and Bosch, M.L.
TITLE Direct Submission
JOURNAL Submitted (14-JUN-1999) Pathobiology, University of Washington, Box
357238, Seattle, WA 98125, USA

FEATURES
source Location/Qualifiers
1..336
/organism="Macaque gamma virus"
/mol_type="genomic DNA"
/strain="Macaque fascicularis 037 gamma virus"
/db_xref="taxon:111468"
<1..>336
/gene="pol"
<1..>336
/gene="pol"
/codon_start=2
/product="DNA polymerase"
/protein_id="AA023087.1"
/db_xref="GI:6671083"
/translation="TWINGRDLHLPITLPDDYETFPVLSGGPVHFKHRSLSLGR
LTVLEKRAIRRTLAACDDPSLTKITLQDLAKVTCNAVYGFYGVASGLPCINIA
ETVTLRGRT"

BASE COUNT 75 a 101 c 107 g 53 t

ORIGIN

Query Match 0.1%; Score 48; DB 1; Length 336;
Best Local Similarity 100.0%; Pred. No. 1.8e-16;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15975 CCTGACGCCGAGCAGCTACGAGCGTCTGCTGAGCGGAGCCGGT 16022
DB 40 CCTGACGCCGAGCAGCTACGAGCGTCTGCTGAGCGGAGCCGGT 87

FEATURES
source Location/Qualifiers
1..336
/organism="Macaque gamma virus"
/mol_type="genomic DNA"
/strain="Macaque fascicularis 040 gamma virus"
/db_xref="taxon:111468"
<1..>336
/gene="pol"
<1..>336
/gene="pol"
/codon_start=2
/product="DNA polymerase"
/protein_id="AA023087.1"
/db_xref="GI:6671083"
/translation="TWINGRDLHLPITLPDDYETFPVLSGGPVHFKHRSLSLGR
LTVLEKRAIRRTLAACDDPSLTKITLQDLAKVTCNAVYGFYGVASGLPCINIA
ETVTLRGRT"

BASE COUNT 75 a 101 c 107 g 53 t

ORIGIN

Query Match 0.1%; Score 48; DB 1; Length 336;
Best Local Similarity 100.0%; Pred. No. 1.8e-16;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15975 CCTGACGCCGAGCAGCTACGAGCGTCTGCTGAGCGGAGCCGGT 16022
DB 40 CCTGACGCCGAGCAGCTACGAGCGTCTGCTGAGCGGAGCCGGT 87

RESULT 14
AF159035
LOCUS AF159035
DEFINITION Macaque gamma virus strain Macaca nemestrina 139 gamma virus DNA
ACCESSION AF159035
VERSION AF159035.1 GI:6671078
KEYWORDS
SOURCE Macaque gamma virus
ORGANISM Macaque gamma virus
VIRUSES; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
REFERENCE
AUTHORS Strand, K., Harper, E., Thormalen, S., Thoulless, M.E., Tsai, C.,
Rose, T. and Bosch, M.L.
TITLE Two distinct lineages of macaque gamma herpesviruses related to the
Kaposi's sarcoma associated herpesvirus
J. Clin. Virol. 16 (3), 253-269 (2000)
JOURNAL 20204465
MEDLINE 10738144
PUBMED 10738144
REFERENCE
AUTHORS Strand, K.B. and Bosch, M.L.
TITLE Direct Submission
JOURNAL Submitted (14-JUN-1999) Pathobiology, University of Washington, Box
357238, Seattle, WA 98125, USA
FEATURES
source
1. .336
Location/Qualifiers
/organism="Maque gamma virus"
/mol_type="genomic DNA"
/strain="Macaque nemestrina 139 gamma virus"
/db_xref="taxon:111468"
<1. .>336
/gene="pol"
<1. .>336
/codon_start=2
/product="DNA polymerase"
/protein_id="AAF23085.1"
/db_xref="GI:6671078"
/translation="TMHGRDLHPLPTDDYETPLSGCPHFVKKHRESLGLT
LTYMLEKRAIRKTLAACDPISLKTIIIDKQOLAIKVCNAVYGTGASGLPCINIA
ETVTLRRT"
BASE COUNT 74 a 103 c 106 g 53 t
ORIGIN
Query Match 0.1%; Score 47; DB 1; Length 336;
Best Local Similarity 100.0%; Pred. No. 6.9e-16;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 15976 CTGACCGCGGAGACTGACGAGCTGCTGCTGAGCGGACCGGT 16022
DB 41 CTGACCGCGGAGACTGACGAGCTGCTGCTGAGCGGACCGGT 87

RESULT 15
SH1DNAPOLA
LOCUS SH1DNAPOLA 3144 bp DNA linear VRL 14-AUG-1995
DEFINITION Pseudorabies virus DNA polymerase gene, partial cds.
ACCESSION L24487
VERSION L24487.1 GI:438894
KEYWORDS DNA polymerase.
SOURCE Pseudorabies virus
ORGANISM Pseudorabies virus
VIRUSES; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicelloviruses.
REFERENCE
AUTHORS Berthomme, H., Monahan, S.J., Parris, D.S., Jacquemont, B. and
Epstein, A.L.
TITLE Cloning, sequencing, and functional characterization of the two
subunits of the pseudorabies virus DNA polymerase holoenzyme:
evidence for specificity of interaction
J. Virol. 69 (5), 2811-2818 (1995)

MEDLINE 95222727
PUBMED 7707503
COMMENT Original
Kaplan) DNA.
FEATURES
source
1. .314
Location/Qualifiers
/organism="Pseudorabies virus"
/mol_type="genomic DNA"
/isolate="Kaplan"
/db_xref="taxon:10345"
<1. .>314
/codon_start=1
/product="DNA polymerase"
/protein_id="AA074383.1"
/db_xref="GI:438895"
/translation="MAROGSVYTRLSSEFKIAPRCIDAPEDRGVHGTIAREPTVYC
GGATRPILRCEPFPFRVNAAMEGAPPEPVPSPREPRFVYDIVESTEVASADPRPNT
VVLGLISACGKRVAVHVGVRHRYFELGKAEDALGASAEQALRALSAAGAPRL
GPADVDARVVDAAPVVYVDARPRPFYEVSSNSGRVHNLRETVCAGLVTEAGVADAT
RLIDHDLPSEGVNRLRPPGAGERVVLVRLHRTSSDVEVCTPLNARDEGPPDYK
LICEFDICRAGDAAFPAAENPEDLVIOISLVSIAVLEHTLFLFSLGSDSDPA
VTVLEPDEPSELLAFTVPLKQYAPAPATGVNIIIPMAVFNKLTIVYGLADGCR
FNGGQPRVYDAGONSQKRSKYKINCLVSLDMYVAAADKLKLPSTYLVAAEALGE
RKLDLDYKDIIPRYAAGPRERGVIGRCVODSALVGLFKFLPHLELVARLANIT
LARAIVDGOIIRVETCLKLAGSKGFLVLPKRRALADEDDGGGOGAKVLEPPSGFRV
DPVILDFASLPSIIQAHNLCEFTTLARPAQIRDEFSAFEVNGSRIFYHAGVRE
SLSTILRDLMARKARIRARIPTSAPPEAVLIDKQAAIRVVCNSVYGFVANGCLP
CLPVAATVTITGRDMLVATRDYOTRATREBELRDIPARPAEYAVRVYVYGTDSV
FTRSGIAYDVCEBGLMARTITRDLPFPPIKLECKTRRLILITKKYITGIVNG
KMLMGVDLVKRNKCAFINAVARLVLDLFEGDEVSAATAITAPARMLERVLPG
FAAFGRVLAHAHARVAGAGLIDVADFPVTAELSRPPAYSVTRLPHTVYVHAKLMRHG
EVPVSKEVSYVITAPPEARDGAVRPGKLVLSDLAEDPRAVYVHAGVPLNTE
YFESHLSLSTLVTFKALFNGDRTKTERLKRFPETAPGDAPFEHFAALTGCGGS
LQTLRTFTCTPAAPRS"
BASE COUNT 463 a 1172 c 1050 g 459 t
ORIGIN
Query Match 0.1%; Score 46; DB 1; Length 3144;
Best Local Similarity 100.0%; Pred. No. 3.5e-15;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 15886 TTTCGACGCTGTACCGGACATCATCCAGCGCACAACCTGTGCT 15931
DB 1720 TTTCGACGCTGTACCGGACATCATCCAGCGCACAACCTGTGCT 1765

Search completed: September 25, 2003, 11:53:05
Job time : 11973 secs

THIS PAGE BLANK (USPTO)